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Amendments to the Specification:

At page 13, lines 16-30, please replace paragraph with the following:

The Expect value is used as a convenient way to create a significance threshold for reporting results. The default value used for blasting is typically set to 0.0001. In BLAST 2.0, the Expect value is also used instead of the P value (probability) to report the significance of matches. For example, an E value of one assigned to a hit can be interpreted as meaning that in a database of the current size one might expect to see one match with a similar score simply by chance. An E value of zero means that one would not expect to see any matches with a similar score simply by chance. See, e.g., <http://www.ncbi.nlm.nih.gov/Education/BLASTinfo/>. Occasionally, a string of X's or N's will result from a BLAST search. This is a result of automatic filtering of the query for low-complexity sequence that is performed to prevent artifactual hits. The filter substitutes any low-complexity sequence that it finds with the letter "N" in nucleotide sequence (e.g., "NNNNNNNNNNNNNNNN") or the letter "X" in protein sequences (e.g., "XXXXXXXXXX"). Low-complexity regions can result in high scores that reflect compositional bias rather than significant position-by-position alignment. (Wootton and Federhen, Methods Enzymol 266:554-571, 1996) (~~Wootton and Federhen, Methods Enzymol 266:554-571, 1996~~).

At page 23, please replace Table 1J with the following:

Table 1J. BLAST results for NOV1a					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 13569928 ref NP_112217.1 NP 112217	a disintegrin-like and metalloprotease with thrombospondin type 1 motif, 12 [Homo sapiens]	1593	269/616 (43%)	371/616 (59%)	e-135
gi 11493589 gb AAG35563.1 AF163762.1 (AF163762) AAG35563	zinc metalloendopeptidase [Homo sapiens]	1077	253/624 (40%)	359/624 (56%)	e-128

gi 10645199 ref NP-055087.1 NP 055087	a disintegrin and metalloprotease with thrombospondin motifs-7 preproprotein; a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 7 [Homo sapiens]	997	247/571 (43%)	344/571 (59%)	e-127
gi 15309931 ref XP-054419.1 XP 054419	a disintegrin-like and metalloprotease domain with thrombospondin type I repeats 10 [Homo sapiens]	854	245/604 (40%)	348/604 (57%)	e-124
gi 7656869 ref NP-055088.1 NP 055088	a disintegrin and metalloprotease with thrombospondin motifs-6 preproprotein; a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 6 [Homo sapiens]	860	244/630 (38%)	345/630 (54%)	e-115

At page 24 please replace Table 1K with the following:

Table 1K. ClustalW Analysis of NOV1

- 1) Novel NOV1a (SEQ ID NO:2)
- 2) Novel NOV1b (SEQ ID NO:4)
- 3) Novel NOV1c (SEQ ID NO:6)
- 4) Novel NOV1d (SEQ ID NO:8)
- 4) ~~gi|13569928|ref|NP-112217.1|~~ ~~gi|13569928|~~ NP 112217 a disintegrin-like and metalloprotease with thrombospondin type 1 motif, 12 [Homo sapiens] (SEQ ID NO:30)
- 5) ~~gi|11493589|gb|AAG35563.1|AF163762.1~~ ~~gi|11493589|~~ AAG35563 (AF163762) zinc metalloendopeptidase [Homo sapiens] (SEQ ID NO:31)
- 6) ~~gi|10645199|ref|NP-055087.1|~~ ~~gi|10645199|~~ NP 055087 a disintegrin and metalloprotease with thrombospondin motifs-7 preproprotein; a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 7 [Homo sapiens] (SEQ ID NO:32)
- 7) ~~gi|15309931|ref|XP-054419.1|~~ ~~gi|15309931|~~ XP 054419 a disintegrin-like and metalloprotease domain with thrombospondin type I repeats 10 [Homo sapiens] (SEQ ID NO:33)
- 8) ~~gi|7656869|ref|NP-055088.1|~~ ~~gi|7656869|~~ NP 055088 a disintegrin and metalloprotease with thrombospondin motifs-6 preproprotein; a disintegrin-like and metalloprotease (reprolysin type) with thrombospondin type 1 motif, 6 [Homo sapiens] (SEQ ID NO:34)

Applicants: Guo
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      10      20      30      40
      |.....|.....|.....|.....|
NOV1a  MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQ
NOV1b  MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQ
NOV1c  -----
NOV1d  MKPRARGWRGLAALWMLLAQVAEQVSPGRSHQRGNRGSGQ
gi |13569928| -----
gi |11493589| -----
gi |10645199| -----
gi |15309931| -----
gi |7656869| -----

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      50      60      70      80
      |.....|.....|.....|.....|
NOV1a  LEASPPRLLSRGPRRLTAMSP LF SAGTCVRHGTRSGSAWE
NOV1b  LEASPPRLLSRGPRRLTAMSP LF SAGTCVRHGTRSGSAWE
NOV1c  -----MGP-----AAAAP-----GSPSV
NOV1d  LEASPPRLLSRGPRRLTAMSP LF SAGTCVRHGTRSGSAWE
gi |13569928| ---MPCAQRSWLANLSVVAQLLNFGALCYGRQPQPGPVRF
gi |11493589| -----
gi |10645199| ---MPGGPSPRSPAPLLRPLLLLLLALAPG-APGPAPGRA
gi |15309931| -----
gi |7656869| -----MEILWKTTLTWILSLIMASSEFHS DHRL

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      90      100      110      120
      |.....|.....|.....|.....|
NOV1a  PERPASSSTRGAAGLDGKGRDMDEAGNHR SQQTNTGTENQ
NOV1b  PERPASSSTRGAAGLDGKGRDMDEAGNHR SQQTNTGTENQ
NOV1c  PRPPP-----
NOV1d  PERPASSSTRGAAGLDGKGRDMDEAGNHR SQQTNTGTENQ
gi |13569928| PDRRQEHFIKGL-----
gi |11493589| --RSQDEF LSSL-----
gi |10645199| TEGR-----
gi |15309931| -----
gi |7656869| SYSSQEEFLTYL-----

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      130      140      150      160
      |.....|.....|.....|.....|
NOV1a  TLHVL T-QYDLVSAYEVDHRC DYVSHEEMHHQR-RRRAVA
NOV1b  TLHVL TREYDLVSAYEVDHRC DYVSHEEMHHQR-RRRAVA
NOV1c  -----DYVSAYEVDHRC DYVSHEEMHHQR-RRRAVA
NOV1d  TLHVL T-QYDLVSAYEVDHRC DYVSHEEMHHQR-RRRAVA
gi |13569928| -----PEYEVVGPVRVDASGHELSYGBHYPITSSRRKRD
gi |11493589| -----ESYEHAFPTTRVDHNGALAFSPPPP-RRORRG TG
gi |10645199| -----AALDTVHPVRVDAGGSELSYELWP--R-ALRKRD
gi |15309931| -----
gi |7656869| -----EHYQETIPIRVDONGAFLSFTVKND-EHSRRRRS

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```

      170      180      190      200
      |.....|.....|.....|.....|
NOV1a  VS-----EVES-LHLRIKGRHDFHMDLRTSSSLVAPGFI
NOV1b  VS-----EVES-LHLRIKGRHDFHMDLRTSSSLVAPGFI
NOV1c  VS-----EVEP-AFLOVCRARELRLCVEAFPIANSQPGFI
NOV1d  VS-----EVES-LHLRIKGRHDFHMDLRTSSSLVAPGFI
gi |13569928| ED-----GSEDW-VYYRISHEEKDLFFNLTVNQGFLSNSYI
gi |11493589| AT-----AESRIIFYKVASPSTHLLNLTSSRLLAGHVS
gi |10645199| VS-----VRRDAPAFYEIQYRGRELRFNTANQHLAPGFI
gi |15309931| -----
gi |7656869| MDPIDPQQAVSKLFFKLSAYGKHFLNLTNTDFVSKHET

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      210      220      230      240
      |.....|.....|.....|.....|

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NOV1a  VQTLGKTKTSVQTLTP--P-EDFCFYQGSLSRSHRNPSPHG
NOV1b  VQTLGKTKTSVQTLTP--P-EDFCFYQGSLSRSHRNPSPHG
NOV1c  NLSNVRSHWREQHASKRII-TNAMLGESALASTRKS---N
NOV1d  VQTLGKTKTSVQTLTP--P-EDFCFYQGSLSRSHRNPSPHG
gi 13569928 MEKR-YGNLSHVKKMMAS--SAPLCHLSGTVLQQGTRVGTA
gi 11493589 VEYWTREGLAHQRAARP-----HCLYAGHGGQASS--HV
gi 10645199 SETRRGGGLGRAHIRAH---TPACHLLGEVQDPELEGGLA
gi 15309931 -----
gi 7656869 VEYWGKDGPPQWKHDFLD-----NCHYTGVLQDQRSIT-KV

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                250      260      270      280
NOV1a  ....|....|....|....|....|....|....|....|
NOV1b  GKFCGSTRTLKLCNSQKCPDSDVDERAAQCAEHNSRRFR
NOV1c  GKFCGSTRTLKLCNSQKCPDSDVDERAAQCAEHNSRRFR
NOV1d  CVFFFL-S---FYFFQSGMIRTEADYFLRPLPSHLSWKLG
gi 13569928 GKFCGSTRTLKLCNSQKCPDSDVDERAAQCAEHNSRRFR
gi 11493589 ALSACHG-----LTGFFQLPHGDFIEFPVKKHPLVEG-
gi 10645199 AISTCGG-----LHGLIVADEEEXYLIEPLHGGPKGS--
gi 15309931 AISACDG-----LKGVFQLSNEDYFIEPLDSAPARPG-
gi 7656869 -----
ALSNCVG-----LHGVIATDEEYFIEPLKNTTDSKH

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                290      300      310      320
NOV1a  ....|....|....|....|....|....|....|....|
NOV1b  GRHYKWKPTQVEADLCKLYCIAEGFDFFFSLSNKKVDGT
NOV1c  GRHYKWKPTQVEADLCKLYCIAEGFDFFFSLSNKKVDGT
NOV1d  RAAQGSSPSHVLYKREVLVTSRTWELAHQPLHSSDLRLGL
gi 13569928 GRHYKWKPTQVEADLCKLYCIAEGFDFFFSLSNKKVDGT
gi 11493589 ----GYHPEIIVYRRQKVP-----ETKEP-ICGLKDSV
gi 10645199 RSPESGPEVYVYKRSSLRHPHLDTACGV-RDEKPKWGRPW
gi 15309931 ----HAQPEVYVYRQAPER---IAQRGDSSAPSICGVQVYP
gi 7656869 -----
FSYENGHPEVIYKKSALQQRHLYDHSCHGVSDFTSRGKPW

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                330      340      350      360
NOV1a  ....|....|....|....|....|....|....|....|
NOV1b  PCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDE
NOV1c  PCSEDSRNVCIDGICE-----MPQPPKEDLFILPDE
NOV1d  PQKHFCGRKK-----YMPQPPKEDLFILPDE
gi 13569928 PCSEDSRNVCIDGICELSVVSTSAHMPQPPKEDLFILPDE
gi 11493589 NISQ-----KQELWREK
gi 10645199 WLRT-----LKPPPARP
gi 15309931 ELES-----RRERWEQR
gi 7656869 -----
WLN-----DTSTVSYS

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                370      380      390      400
NOV1a  ....|....|....|....|....|....|....|....|
NOV1b  YKSLRHKRSILRSHRNEELNVETLVVVDKMMONHGHEN
NOV1c  YKSLRHKRSILRSHRNEELNVETLVVVDKMMONHGHEN
NOV1d  YKSLRHKRSILRSHRNEELNVETLVVVDKMMONHGHEN
gi 13569928 YKSLRHKRSILRSHRNEELNVETLVVVDKMMONHGHEN
gi 11493589 WERHNLPSRSLSRRSISKRWVETLVVADTKMVEYHGSN
gi 10645199 LGNETERGQPLKRSVSRERYVETLVVADKMMVAYHGRRD
gi 15309931 QQWRRPRLRRIHORSVSKRWVETLVVADKMMVEYHQPQ
gi 7656869 -----MMVAYHGRRD
LPINNTHIHHROKRSVETIRFVETLVVADKMMVGYHGRRD

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                410      420      430      440
NOV1a  ....|....|....|....|....|....|....|....|
NOV1b  HTTYVLTITNMVSALFKDGTGG-----NNINIAIVGLILL
NOV1c  HTTYVLTITNMVSALFKDGTGG-----NNINIAIVGLILL
NOV1d  HTTYVLTITNMVSALFKDGTGG-----NNINIAIVGLILL
gi 13569928 HTTYVLTITNMVSALFKDGTGG-----NNINIAIVGLILL
gi 11493589 HTTYVLTITNMVSALFKDGTGG-----NNINIAIVGLILL
gi 10645199 HTTYVLTITNMVSALFKDGTGG-----NNINIAIVGLILL
gi 15309931 HTTYVLTITNMVSALFKDGTGG-----NNINIAIVGLILL
gi 7656869 HTTYVLTITNMVSALFKDGLMGKDGTRHDHAILTGLDTC

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gi|13569928| VESYVLTITAMVVTGLFHNPSIGN-----ATHTVMVRITILL
gi|11493589| VEQYVLATAMNIVAKLFODSSIGS-----TUNILVTRITILL
gi|10645199| VESYVLTITAMVAGLEHDPSTIGN-----PIHTITVRLVILL
gi|15309931| VEQYVLATAMNIVAKLFODSSIGS-----TUNILVTRITILL
gi|7656869| DEHYVLSVAMNIVAKLYRDSIGN-----VUNILVARITILL
```

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450      460      470      480
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a    EDEOPGLVISHHADHTLSSFCQWQSGMKGKD-----
NOV1b    EDEO-----
NOV1c    EDEOPGLVISHHADHTLSSFCQWQSGMKGKD-----
NOV1d    SWKN-----
gi|13569928| EEEKQGLKIVHHAETLSSFCQWQKSINPKS-----DL
gi|11493589| TEDOPTLETTHHAGKSLDSFCQWQKSTVNHSGHGNAIPEN
gi|10645199| EDEEEDLKITHHADNTEKSFCKWQKSINMKG-----DA
gi|15309931| TEDOPTLETTHHAGKSLDSFCQWQKSTVNHSGHGNAIPEN
gi|7656869| TEDOPNLETNNHADKSLDSFCQWQKSILLSHQSDGNTIPEN
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490      500      510      520
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a    --TRHDHAILLTGLDICSWNKEPCDTLGFAPISGMCCKYR
NOV1b    -----
NOV1c    --TRHDHAILLTGLDICSWNKEPCDTLGFAPISGMCCKYR
NOV1d    -----EPCDTLGFAPISGMCCKYR
gi|13569928| NPVEHDAVALLTRKDICAGFNRPCEITGLSHLSGMCQPER
gi|11493589| GVANHDAVALLTRYDICTYKPKPCGTLGLAPVGGMCERER
gi|10645199| HPLEHDAVALLTRKDICAAMNRPCEITGLSHVAGMCQPER
gi|15309931| GVANHDAVALLTRYDICTYKPKPCGTLGLAPVGGMCERER
gi|7656869| GIAHDAVALLTRYDICTYKPKPCGTLGLASVAGMCEPER
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530      540      550      560
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a    SCTINEDTGLGLAFTIAHESGHNFGMHDCGGMCKKSEG
NOV1b    -----
NOV1c    SCTINEDTGLGLAFTIAHESGHNFGMHDCGGMCKKSEG
NOV1d    SCTINEDTGLGLAFTIAHESGHNFGMHDCGGMCKKSEG
gi|13569928| SCTINEDSGLPPLAFTIAHELGHSEFGIHDCKENDCEPVGR
gi|11493589| SCSYNEDIGLPOAFTIAHELGHSEFGIHDCKENDCEPVGR
gi|10645199| SCSYNEDTGLPLAFTIAHELGHSEFGIHDCKENDCEPVGR
gi|15309931| SCSYNEDIGLATAFTIAHELGHSEFGIHDCKENDCEPVGR
gi|7656869| SCSYNEDIGLGSFTIAHEIVHNEFGMNDGICNSGCRK--
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570      580      590      600
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a    N---DMSPTLAGRNQVSWSPCSRQYVHKFLSTAQAICLA
NOV1b    -----
NOV1c    N---DMSPTLAGRNQVSWSPCSRQYVHKFLSTAQAICLA
NOV1d    N---DMSPTLAGRNQVSWSPCSRQYVHKFLSTAQAICLA
gi|13569928| HP-YIMSRQLQYDPTPLTWSKCSSEYITRFLDRGWGFLD
gi|11493589| DPAKQMAAHTMTNPFVWSSCSRQYITSEFDSGLGLCIN
gi|10645199| RP-FIMSPQLLYDAAPLTWSRCSRQYITRFLDRGWGFLD
gi|15309931| DPAKQMAAHTMTNPFVWSSCSRQYITSEFDSGLGLCIN
gi|7656869| -----VMKQQNYG-SSHYCEYQSFEL-----VCLQ
```

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610      620      630      640
.....|.....|.....|.....|.....|.....|.....|.....|
NOV1a    DQPKPVKEYKYPEKLPGEIYDANTQCKWQFGEKAKLCMLD
NOV1b    -----
NOV1c    DQPKPVKEYKYPEKLPGEIYDANTQCKWQFGEKAKLCMLD
NOV1d    DQPKPVKEYKYPEKLPGEIYDANTQCKWQFGEKAKLCMLD
gi|13569928| DIPKK-KGLKSKVIAPGVIYDVHHQCQLQYQ--PNATFCQ
gi|11493589| NRPPR-QDFVYPTVAPGQAYDAEQCRFOH---GVKSRQC
gi|10645199| DPPAK-DIIDEPSVPPGVLYDVSHQCRLQYQ--AYSAPCE
gi|15309931| NRPPR-QDFVYPTVAPGQAYDAEQCRFOH---GVKSRQC
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gi|7656869| SRX-----HHQ

	650	660	670	680
NOV1a	FKKDI	CKALW	CHRIGR	KCEIKFMPAAEGTHCG---HDMW
NOV1b	---	DI	CKALW	CHRIGR
NOV1c	FKKDI	CKALW	CHRIGR	KCEIKFMPAAEGTHCG---HEHG
NOV1d	FKKDI	CKALW	CHRIGR	KCEIKFMPAAEGTHCG---HDMW
gi 13569928	EVENV	CQTLW	CSVKG-	FCRSKLDAAAGTCCG---EKNW
gi 11493589	KYGEV	CSELW	CLS	SKSNRCITNSIPAAEGTHCQTHTIDKGW
gi 10645199	DMDNV	CHTLW	CSVGT-	TCHSKLDAAVDGTCCG---ENKW
gi 15309931	KYGEV	CSELW	CLS	SKSNRCITNSIPAAEGTHCQTHTIDKGW
gi 7656869	LFREVC	RELW	CLS	SKSNRCITNSIPAAEGTHCQTNIEKGW

	690	700	710	720
NOV1a	CRGGOC	CVKYG	DEGPK	PTHGHWSDWSSWSPCSRTC
NOV1b	CRGGOC	CVKYG	DEGPK	PTHGHWSDWSSWSPCSRTC
NOV1c	A-GGOC	CVKYG	DEGPK	PTHGHWSDWSSWSPCSRTC
NOV1d	CRGGOC	CVKYG	DEGPK	PTHGHWSDWSSWSPCSRTC
gi 13569928	CMAGK	CHTV	CKK-	PE
gi 11493589	CYKRV	CVPE	CSR-	PEGVD
gi 10645199	CLS	GEC	VPV	GFR-
gi 15309931	CYKRV	CVPE	CSR-	PEGVD
gi 7656869	CYQGD	CVPE	GTW-	POSID

	730	740	750	760
NOV1a	RSR-	LCTNP	NP	SHGGKE
NOV1b	RSR-	LCTNP	PRP	SHGGKE
NOV1c	RSR	QNT	HSR	P
NOV1d	RSR-	LCTNP	NP	SHGGKE
gi 13569928	AER-	L	CNN	PE
gi 11493589	SSR-	H	CD	S
gi 10645199	AER-	Q	CTO	P
gi 15309931	SSR-	H	CD	S
gi 7656869	SLR-	H	CD	S

	770	780	790	800
NOV1a	RAAQCA	EHNSRR	FRGREY	KWKPE---
NOV1b	RAAQCA	EHNSRR	FRGREY	KWKPE---
NOV1c	RAAQCA	EHNSRR	FRGREY	KWKPE---
NOV1d	RAAQCA	EHNSRR	FRGREY	KWKPE---
gi 13569928	ROMQC	SEF	DTVP	YK
gi 11493589	REVQC	SEF	DSIP	FRG
gi 10645199	RHVQC	SHF	D	AML
gi 15309931	REVQC	SEF	DSIP	FRG
gi 7656869	REKQC	AD	FD	NMP

	810	820	830	840
NOV1a	EDFFFS	LSNKVK	DGTPCS	--EDSRNV
NOV1b	EDFFFS	LSNKVK	DGTPCS	--EDSRNV
NOV1c	EDFFFS	LSNKVK	DGTPCS	--EDSRNV
NOV1d	EDFFFS	LSNKVK	DGTPCS	--EDSRNV
gi 13569928	GQF	SEK	ML	DA
gi 11493589	ENFYTER	AAAV	DGTPCR	--PD
gi 10645199	EYFAK	TER	AAAV	DGTPC
gi 15309931	ENFYTER	AAAV	DGTPCR	--PD
gi 7656869	ENFYTER	AAAV	DGTPC	--AD

	850	860	870	880

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NOV1a  LGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTN-YYHMY
NOV1b  LGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTN-YYHMY
NOV1c  LGSDAVEDVCGVCNGNNSACTIHRGLY---LE---YYHMY
NOV1d  LGSDAVEDVCGVCNGNNSACTIHRGLYTKHHHTNYYHMY
gi | 13569928 | LIDSNATEDRCGVCLGDGSSCQTVRKMEKQKE-GSGYVDIG
gi | 11493589 | LGSDLREDKCRVCGGSGSACETIEGVSPASPGAGYEDVV
gi | 10645199 | LIDSGAMEDRCGVCHGNGSTCHTVSGTEEEAE-GLGYVDVG
gi | 15309931 | LGSDLREDKCRVCGGSGSACETIEGVSPASPGAGYEDVV
gi | 7656869 | LGSDAREDRCRVCGGGGSGTCDATIEGFENDSLPRGGYMEVV

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```

      890      900      910      920
.....|.....|.....|.....|
NOV1a  TIPSGARSIRIYEMNVSTSYGSRVN-ALRYYLNGHWTVQ
NOV1b  TIPSGARSIRIYEMNVSTSYGSRVN-ALRYYLNGHWTVQ
NOV1c  TIPSGARSIRIYEMNVSTSYGSRVN-ALRYYLNGHWTVQ
NOV1d  TIPSGARSIRIYEMNVSTSYGSRVN-ALRYYLNGHWTVQ
gi | 13569928 | LIPKCARDIRVMEIEGAGNEPAIRSEDPEKYYLNGGFTIQ
gi | 11493589 | WIPKGSVHIFLODNLSLSHLALKGDQ-ESLLLEGLPGTP
gi | 10645199 | LIPAGAREIRIOEVAEPAANELAIRSEDPEKYYLNGGFTIQ
gi | 15309931 | WIPKGSVHIFLODNLSLSHLALKGDQ-ESLLLEGLPGTP
gi | 7656869 | QIPRGSVHIEVREVAASKNYALKSEG-DDYYLNGAWTVQ

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      930      940      950      960
.....|.....|.....|.....|
NOV1a  WPGRYKFSGTTEDYRRSYNEPENLIATGPTNETLIVETLF
NOV1b  WPGRYKFSGTTEDYRRSYNEPENLIATGPTNETLIVETLF
NOV1c  WPGRYKFSGTTEDYRRSYNEPENLIATGPTNETLIVETLF
NOV1d  WPGRYKFSGTTEDYRRSYNEPENLIATGPTNETLIVETLF
gi | 13569928 | WNGNYKLACTVFOYDRKGD-LEKLMAATGPTNESVWLOTLF
gi | 11493589 | QPHERLPLAGTTFQLRQGPQVQSLEALGPTNASLIVMVLA
gi | 10645199 | WNGDYQVAGTTFYARRGN-WENLTSPGETKEPWVIG---
gi | 15309931 | QPHERLPLAGTTFQLRQGPQVQSLEALGPTNASLIVMVLA
gi | 7656869 | WPRKEDVAGTAFHYKRPTDEPESLEALGPTSENLIIVMVL

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      970      980      990      1000
.....|.....|.....|.....|
NOV1a  QGRNPGVAWEYS-----
NOV1b  QGRNPGVAWEYS-----
NOV1c  QGRNPGVAWEYS-----
NOV1d  QGRNPGVAWEYS-----
gi | 13569928 | QVTNPGGKKMXTIQKDGLDNDVEQMYFWQYGHWTECSVTC
gi | 11493589 | RTELPAIRRRFN-----
gi | 10645199 | -----
gi | 15309931 | RTELPAIRRRFN-----
gi | 7656869 | QEONLGRYRKN-----

```

```

      1010      1020      1030      1040
.....|.....|.....|.....|
NOV1a  -----
NOV1b  -----
NOV1c  -----
NOV1d  -----
gi | 13569928 | GTGIRRQTAHCIKKGRGMVKATFCDPETQPNGRQKKCHEK
gi | 11493589 | -APIAR-----DS
gi | 10645199 | ---VP-----
gi | 15309931 | -APIAR-----DS
gi | 7656869 | -VPITRTGSG-----DN

```

```

      1050      1060      1070      1080
.....|.....|.....|.....|
NOV1a  -----MPRLGTE-----
NOV1b  -----MPRLGTE-----
NOV1c  -----MPRLGTE-----
NOV1d  -----MPRLGTE-----

```


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```
gi|13569928|ACPPRWAGEWEACSATCGPHGEKKRTVLCIQTMVSDEQA
gi|11493589|LPPYSWHYAPWTKCSAQAGGSQV-QAVECRNQL--DSSA
gi|10645199|-----ASRGPGGGS-R-----GG
gi|15309931|LPPYSWHYAPWTKCSAQAGGSQV-QAVECRNQL--DSSA
gi|7656869|EVGFTWNHQPWSECSATCAGG-----
```

```

1090      1100      1110      1120
....|....|....|....|....|....|....|....|
NOV1a     KOPPAOPS
NOV1b     KOPPAOPS
NOV1c     KOPPAOPS
NOV1d     KOPPAOPS
gi|13569928|LPPTDCQ-HLLKPKTLLSCNRDILCPDWTVGWNSSECSVS
gi|11493589|VAPHYCSAHSKLPKRQRCNTEP-CPPDWVVGWNSLCSRS
gi|10645199|VP-----EPSTLHGRSR-----P---
gi|15309931|VAPHYCSAHSKLPKRQRCNTEP-CPPDWVVGWNSLCSRS
gi|7656869|-----KMPTRQ-----P-----TQR
```

```

1130      1140      1150      1160
....|....|....|....|....|....|....|....|
NOV1a     YLWATVR
NOV1b     YLWATVR
NOV1c     YLWATVR
NOV1d     YLWATVR
gi|13569928|CGGGVRIKSVTCAKNHDEPCDVTRKPNRSLCGLQQCPS
gi|11493589|CDAGVRERSVVCQR-----
gi|10645199|--GGVSPGSGT-----E-PGS-----
gi|15309931|CDAGVRERSVVCQR-----
gi|7656869|--ARWRKHHHSY-----
```

```

1170      1180      1190      1200
....|....|....|....|....|....|....|....|
NOV1a
NOV1b
NOV1c
NOV1d
gi|13569928|RRVLKPNKGTISNGKNPPTLKPVPPTSRPRMLTPTGPE
gi|11493589|-----RVSAAEKALDDSAACQ-----
gi|10645199|-----EPGPPAAAS-----
gi|15309931|-----RVSAAEKALDDSAACQ-----
gi|7656869|-----ALCLLKKLIGNISCR-----
```

```

1210      1220      1230      1240
....|....|....|....|....|....|....|....|
NOV1a     SECSVSCGGGRC
NOV1b     SECSVSCGGGRC
NOV1c     SECSVSCGGGRC
NOV1d     SECSVSCGGGRC
gi|13569928|SMSTSTPAISSPSPTTASKEGDLGGKQWQDS--STQPELS
gi|11493589|---PRPPVLEACHGPTCPPEW--AALDWSECTPSCGPCLR
gi|10645199|-T-SVSPSLKWPNLVAAVHRG-----GWCQA--PLGLCGW
gi|15309931|---PRPPVLEACHGPTCPPEW--AALDWSECTPSCGPCLR
gi|7656869|-----FAS--SCN--LA
```

```

1250      1260      1270      1280
....|....|....|....|....|....|....|....|
NOV1a     LPVLLLEACQPSATAYIALFLES-----
NOV1b     LPVLLLEACQPSATAYIALFLES-----
NOV1c     LPVLLLEACQPLATAYIALFLES-----
NOV1d     LPVLLLEACQPSATAYIALFLES-----
gi|13569928|SRYLLSTGTSQPIILTSQSLSIQPSEENVSSDTGPTSEG
gi|11493589|HRVLLCRSADHRATLPPAHCSPAAKP-----
gi|10645199|RRHLVLMG---PRLPTQLLFQE-----SNP
gi|15309931|HRVLLCRSADHRATLPPAHCSPAAKP-----
```

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```
gi|7656869| KET[REDACTED]-----
                                1290      1300      1310      1320
                                ....|....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi|13569928| GLVATTTSGSGLSSSRNPITWPVTPFYNTLTRGP[REDACTED]EHS
gi|11493589| -----PAT
gi|10645199| G-----VHYEYT-----IHR
gi|15309931| -----PAT
gi|7656869| -----

                                1330      1340      1350      1360
                                ....|....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi|13569928| GSGEEREQPEDKDESNPVIWTKIRVPGNDAPVEST[REDACTED]PLA
gi|11493589| MRCNLRRCPP-----
gi|10645199| EAGGHDEVPP-----
gi|15309931| MRCNLRRCPP-----
gi|7656869| -----

                                1370      1380      1390      1400
                                ....|....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi|13569928| PPLTPDLSRESWWPPFSTVMEGLLPSQRPTTSETGT[REDACTED]RVE
gi|11493589| -----
gi|10645199| -----
gi|15309931| -----
gi|7656869| -----

                                1410      1420      1430      1440
                                ....|....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi|13569928| GMVTEKPANTLLPLGGDEHQPEPSGKTANRNHLKLPNNMNQ
gi|11493589| -----
gi|10645199| -----
gi|15309931| -----
gi|7656869| -----

                                1450      1460      1470      1480
                                ....|....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi|13569928| TKSSEPVLTEEDATSLITEGFLLNASNYKQLTNGHGS[REDACTED]HW
gi|11493589| -----ARW
gi|10645199| -----PVFS-----W
gi|15309931| -----ARW
gi|7656869| -----

                                1490      1500      1510      1520
                                ....|....|....|....|....|....|....|....|
```

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```

NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi | 13569928 | IVGNWSECSTTCGLGAYWKRVECTTQMDSDCAAIRPDPA
gi | 11493589 | VAGEWGECSAQCGVGQRQRSVRCTS-----
gi | 10645199 | HYGPTWKCTVTCGRGE-----
gi | 15309931 | VAGEWGECSAQCGVGQRQRSVRCTS-----
gi | 7656869 | -----

```

```

                1530      1540      1550      1560
                ....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi | 13569928 | KRCHLRPCAGWKVGNWSKCSRNCSSGGFKIREIQCVDSRDH
gi | 11493589 | -----HTGQASHECTEALR-----
gi | 10645199 | -----KWGRHSPTCRG-----LVSGQGH
gi | 15309931 | -----HTGQASHECTEALR-----
gi | 7656869 | -----

```

```

                1570      1580      1590      1600
                ....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi | 13569928 | RNLRPFHQCFLAGIPPPLSMSCNPEPCEAQWQVEPWSQCSR
gi | 11493589 | -----PPTTQQCEA
gi | 10645199 | -----WLQLPA
gi | 15309931 | -----PPTTQQCEA
gi | 7656869 | -----

```

```

                1610      1620      1630      1640
                ....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi | 13569928 | SCGGGVQBRGVFCPGGLCDWTKRPTSTMSCNEHLCCHWAT
gi | 11493589 | KCDS-----PTPG
gi | 10645199 | HC-----WAT
gi | 15309931 | KCDS-----PTPG
gi | 7656869 | -----

```

```

                1650      1660      1670      1680
                ....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----
gi | 13569928 | GNWDLCTSCGGGFQKRIVQCVPSSEGNKTEDQDQCLCDHK
gi | 11493589 | DGPEECKDVN-----
gi | 10645199 | TGLEVCFS-----E-----
gi | 15309931 | DGPEECKDVN-----
gi | 7656869 | -----

```

```

                1690      1700      1710      1720
                ....|....|....|....|....|....|....|
NOV1a -----
NOV1b -----
NOV1c -----
NOV1d -----

```

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```
gi|13569928|PRPPEFKKCNQQACKKSADLLCTKDKLSASFCQTLKAMKK
gi|11493589|-----KVAYCPLVLKFQF
gi|10645199|---P-----QF-----S-ICEMRLAIAL
gi|15309931|-----KVAYCPLVLKFQF
gi|7656869|-----
```

```

              1730      1740      1750
          ....|....|....|....|....|....|...
NOV1a      -----(SEQ ID NO:2 )
NOV1b      -----(SEQ ID NO:4 )
NOV1c      -----(SEQ ID NO:6 )
NOV1d      -----(SEQ ID NO:8 )
gi|13569928|CSVPTVRAECCFSCPQTHITHTQRQRRLQKSKEL(SEQ ID NO:30 )
gi|11493589|CSRAYFRQMCCKTCQGH----- (SEQ ID NO:31 )
gi|10645199|CPRPAGRVHG----- (SEQ ID NO:32 )
gi|15309931|CSRAYFRQMCCKTCHGH----- (SEQ ID NO:33 )
gi|7656869|----- (SEQ ID NO:34 )
```

At page 32, please replace paragraph at lines 31-42 with the following new paragraph:

The presence of identifiable domains in NOV1, as well as all other NOVX proteins, was determined by searches using software algorithms such as PROSITE, DOMAIN, Blocks, Pfam, ProDomain, and Prints, and then determining the Interpro number by crossing the domain match (or numbers) using the European Bioinformatics Institute Interpro website (<http://www.ebi.ac.uk/interpro>). DOMAIN results for NOV1 as disclosed in Tables 1L-IO, were collected from the Conserved Domain Database (CDD) with Reverse Position Specific BLAST analyses. This BLAST analysis software samples domains found in the Smart and Pfam collections. For Table 1E and all successive DOMAIN sequence alignments, fully conserved single residues are indicated by black shading or by the sign (!) and “strong” semi-conserved residues are indicated by grey shading or by the sign (+). The “strong” group of conserved amino acid residues may be any one of the following groups of amino acids: STA, NEQK (SEQ ID NO: 161), NHQK (SEQ ID NO: 162), NDEQ (SEQ ID NO: 163), QHRK (SEQ ID NO: 164), MILV (SEQ ID NO: 165), MILF (SEQ ID NO: 166), HY, FYW.

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Table 1N. Domain Analysis of NOV1

~~gnl|Pfam|pfam00090~~, tsp_1, Thrombospondin type 1 domain. (SEQ ID NO:78)
CD-Length = 48 residues, 100.0% aligned
Score = 54.7 bits (130), Expect = 2e-08

Query: 669 SDWSSWSPCSRTCGGGVSHRSRLCTNPNSHGGKFCEGSTRTLKLCNSQKC 719 (of SEQ ID NO:2)
| | | | | | | | | + | | | + | | | | + + | |
Sbjct: 1 SPWSEWSPCSVTGKGIRTRQRTCNSP---AGGKPCTGDAQETEACMMDPC 48 (SEQ ID NO:78)

At page 34, please replace Table 1O with the following:

Table 1O. Domain Analysis of NOV1

~~gnl|Pfam|pfam01562~~, Pep_M12B_propep, Reprolysin family propeptide.
This region is the propeptide for members of peptidase family M12B.
The propeptide contains a sequence motif similar to the "cysteine switch" of the matrixins. This motif is found at the C terminus of the alignment but is not well aligned. repeats. (SEQ ID NO:79)
CD-Length = 117 residues, only 39.3% aligned
Score = 38.5 bits (88), Expect = 0.002

Query: 180 LRTSSSLVAPGFIVQTLGKTGKTSVQTLPPEDFCFYQGSRLRSHRNS 225 (of SEQ ID NO:2)
| + | | + | | | | | | + + | + | | + + | |
Sbjct: 2 LEKNRSL LAPDFTVTYDDGTLVTEHPLIQDHCYYQGYVEGY PNS 47 (SEQ ID NO:79)

At page 41 please replace Table 2C with the following:

Table 2C. BLAST results for NOV2

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 14765710 ref XP-006925.4 XP 006925	alpha 2 macroglobulin precursor [Homo sapiens]	1474	593/1486 (39%)	870/1486 (57%)	0.0
gi 4557225 ref NP-00005.1 NP 00005	alpha 2 macroglobulin precursor [Homo sapiens]	1474	591/1486 (39%)	869/1486 (57%)	0.0
gi 224053 prf 1009174A- 1009174A	macroglobulin alpha2 [Homo sapiens]	1450	585/1471 (39%)	861/1471 (57%)	0.0

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<u>gi 6978425 ref NP_036620.1 </u> NP 036620	alpha-2-macroglobulin [Rattus norvegicus]	1472	578/1483 (38%)	867/1483 (57%)	0.0
<u>gi 2144118 pir JC5143</u>	alpha-macroglobulin precursor - guinea pig	1476	570/1495 (38%)	858/1495 (57%)	0.0

At page 41 please replace Table 2D with the following:

Table 2D. ClustalW Analysis of NOV2

- 1) NOV2 (SEQ ID NO:10)
- 2) gi|14765710|ref|XP_006925.4| gi|14765710| XP 006925 alpha 2 macroglobulin precursor [Homo sapiens] (SEQ ID NO:35)
- 2) gi|4557225|ref|NP_000005.1| gi|4557225| NP 000005 alpha 2 macroglobulin precursor [Homo sapiens] (SEQ ID NO:36)
- 3) gi|224053|prf|1009174A gi|224053| 1009174A macroglobulin alpha2 [Homo sapiens] (SEQ ID NO:37)
- 4) gi|6978425|ref|NP_036620.1| gi|6978425| NP 036620 alpha-2-macroglobulin [Rattus norvegicus] (SEQ ID NO:38)
- 5) gi|2144118|pir|JC5143 gi|2144118| JC5143 alpha-macroglobulin precursor - guinea pig (SEQ ID NO:39)

	570	580	590	600
NOV2			
gi 14765710	SLVIYAHFPGSGGVADKIQSVEMCFDN-----OOL			
gi 4557225	RLLIYAVLPAGDVIGDSAKYQVENCLANKVDLSFSPSQSL			
gi 224053	RLLIYAVLPAGDVIGDSAKYQVENCLANKVDLSFSPSQSL			
gi 6978425	RLVIYAVLPAGDVIGDSAKYQVENCLANKVDLSFSPSQSL			
gi 2144118	RLVIYAVLPAGDVIGDSAKYQVENCLANKVDLSFSPSQSL			
	610	620	630	640
NOV2			
gi 14765710	PGAEVELQQAAPGSCALRAVDLSVLLRPPDRELSNRSV			
gi 4557225	PASEAHLRVTAAPQSVCALRAVDQSVLLMKPDAELSASSV			
gi 224053	PASEAHLRVTAAPQSVCALRAVDQSVLLMKPDAELSASSV			
gi 6978425	PASEAHLRVTAAPQSVCALRAVDQSVLLMKPDAELSASSV			
gi 2144118	PASKTHLRVTASQPSVSCALRAVDQSVLLMKPDAELSASSV			
	650	660	670	680
NOV2			
gi 14765710	YGLLPEKDLTGFPGLNDQDNE-----CENR			
gi 4557225	YGLLPEKDLTGFPGLNDQDNE-----CENR			
gi 224053	YGLLPEKDLTGFPGLNDQDNE-----CENR			
gi 6978425	YGLLPEKDLTGFPGLNDQDNE-----CENR			
gi 2144118	YGLLPEKDLTGFPGLNDQDNE-----CENR			
	690	700	710	720
NOV2			
gi 14765710	GSSQSRSLIRPFSFSEG-TDLSFFRDVGLKILSNKIRK			
gi 4557225	ENVYINGITYIPVSSSTNEKDMYSFLEDMGLKAFTNSKIRK			
gi 224053	ENVYINGITYIPVSSSTNEKDMYSFLEDMGLKAFTNSKIRK			
gi 6978425	ENVYINGITYIPVSSSTNEKDMYSFLEDMGLKAFTNSKIRK			
gi 2144118	ENVYINGITYIPVSSSTNEKDMYSFLEDMGLKAFTNSKIRK			

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```

      730      740      750      760
      |.....|.....|.....|.....|
NOV2  |PVDCHSRSPPEYST---AMCGGGHPAFESSTP---
gi 14765710 |PKMCPOLQOYEMHGPEGIRVGEYESDVMGRCHARIVHV--
gi 4557225 |PKMCPOLQOYEMHGPEGIRVGEYESDVMGRCHARIVHV--
gi 224053 |PKMCPOLQOYEMHGPEGIRVGEYESDVMGRCHARIVHV--
gi 6978425 |PKVCERLDNKGIPAAYHLVQSMDAFLE-----
gi 2144118 |POLCAHVOKTEVP---TMAYSVSESSSFRSGPRRVPVAVGI

```

```

      770      780      790      800
      |.....|.....|.....|.....|
NOV2  |---LHQAEASQVROYFPETWIWDLFPFGNSCKEAVHVTVP
gi 14765710 |---EEPHETETVRKYFPETWIWDLVVVNSAGVAEVGVTVP
gi 4557225 |---EEPHETETVRKYFPETWIWDLVVVNSAGVAEVGVTVP
gi 224053 |---EEPHETETVRKYFPETWIWDLVVVNSAGVAEVGVTVP
gi 6978425 |S---SESPETETRRSYFPETWIWDLVVVNSAGVAEVEVTVP
gi 2144118 |AATYS EPPKETVRTYSPETWIWDLKVTDSGVAEVEVTVP

```

```

      810      820      830      840
      |.....|.....|.....|.....|
NOV2  |DAITEWKAMSFCTISQSRGFGHSPTVGLTAFKPFVVDLTP
gi 14765710 |DTITEWKAGAFCLSEDAGLGCHSSTASLRAFQFFFVELTMP
gi 4557225 |DTITEWKAGAFCLSEDAGLGCHSSTASLRAFQFFFVELTMP
gi 224053 |DTITEWKAGAFCLSEDAGLGCHSSTASLRAFQPFEEVELTMP
gi 6978425 |DTITEWKAGAFCLSDNTGLGCHSPVVQFAQFQFFFVELTMP
gi 2144118 |DTITEWKAGAFCLSDNTGLGCHSPTASLRAFQFFFVELTMP

```

```

      850      860      870      880
      |.....|.....|.....|.....|
NOV2  |YSVVRGSESERLTATEFNLYLDCIRVQTDLAKSHEVQLESW
gi 14765710 |YSVIRGEAFTLKATVLNLYLPK CIRVSVQLEASPAFLAVPV
gi 4557225 |YSVIRGEAFTLKATVLNLYLPK CIRVSVQLEASPAFLAVPV
gi 224053 |YSVIRGEAFTLKATVLNLYLPK CIRVSVQLEASPAFLAVPV
gi 6978425 |YSVIRGEAFTLKATVLNLYLPTCIRVSVQLEASPDFLAAPE
gi 2144118 |YSVIRGEAFTLKATVLNLYLPDCIRVSVQLEASPKFLAEPK

```

```

      890      900      910      920
      |.....|.....|.....|.....|
NOV2  |ADSOTSSCLCADDKTHHWNTTAVKLGHNFTTISTIKILDS
gi 14765710 |EKEQAPHCI CANGROTVSWAVTPKSLGNVNETVSAEALDS
gi 4557225 |EKEQAPHCI CANGROTVSWAVTPKSLGNVNETVSAEALDS
gi 224053 |EKEQAPHCI CANGROTVSWAVTPKSLGNVNETVSAEALDS
gi 6978425 |EKEQASHCI CMNORHTASWAVTPKSLGNVNETVSAEALNS
gi 2144118 |AKEQESSLCVCGNEROTVSWVTPKSLGNVNETVSAEALDS

```

```

      930      940      950      960
      |.....|.....|.....|.....|
NOV2  |NEPCGGGKGFVPQKGRSDTIKPLLVKPEGVLVEKTHESL
gi 14765710 |QELCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTFNSL
gi 4557225 |QELCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTFNSL
gi 224053 |QELCGTEVPSVPEHGRKDTVIKPLLVEPEGLEKETTFNSL
gi 6978425 |QELCGNEVPVPEQGGKDTTIKSLLVPEGLENEVTTFNSL
gi 2144118 |SELCGNEKTVVPTVGRKDTTIKPLLVEPEGLEKETTFNSL

```

```

      970      980      990     1000
      |.....|.....|.....|.....|
NOV2  |LCPKGGGVASESVSLGLPVDIVPESTKAMVIVLGDILGSA
gi 14765710 |LCPSGGEVSEELSLKLPPNVVEESARASVSVLGDILGSA
gi 4557225 |LCPSGGEVSEELSLKLPPNVVEESARASVSVLGDILGSA
gi 224053 |LCPSGGEVSEELSLKLPPNVVEESARASVSVLGDILGSA
gi 6978425 |LCPMGAEVSEELSLKLPPNVVEESARASVSVLGDILGSA
gi 2144118 |NRVSDTTVSEELSLKLPPNVVQDSARASVSVLGDILGSA

```

1010 1020 1030 1040

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```
.....|.....|.....|.....|.....|.....|.....|.....|
NOV2      |MONTLDGLVQMPSCGGEONMVLFPAPITTYVLOVLEKAGLLTE
gi 14765710|MONTQNLLQMPYGCGEONMVLFPAPNIYVLDYLNETOQLTP
gi 4557225 |MONTQNLLQMPYGCGEONMVLFPAPNIYVLDYLNETOQLTP
gi 224053 |MONTQNLLQMPYGCGEONMVLFPAPNIYVLDYLNETOQLTP
gi 6978425 |MONTQDLLQMPYGCGEONMVLFPAPNIYVLDYLNETOQLTP
gi 2144118 |MONTQNLLQMPYGCGEONMVLFPAPNIYVLDYLNETOQLTP
```

```
.....|.....|.....|.....|.....|.....|.....|.....|
1050      |1060      |1070      |1080
NOV2      |EIKSRAVGELEITGYQKELMYKHSNGSYSAFGERDGL--NGN
gi 14765710|EIKSKAIGYLNITGYORQLNYKHYDGSYSTFGERYGRNOGN
gi 4557225 |EIKSKAIGYLNITGYORQLNYKHYDGSYSTFGERYGRNOGN
gi 224053 |EIKSKAIGYLNITGYORQLNYKHYDGSYSTFGERYGRNOGN
gi 6978425 |EIKSKAIGYLNITGYORQLNYKHYDGSYSTFGERYGRNOGN
gi 2144118 |EIKSKAIGYLNITGYORQLNYKHYDGSYSTFGERYGRNOGN
```

```
.....|.....|.....|.....|.....|.....|.....|.....|
1090      |1100      |1110      |1120
NOV2      |TWLTAFLVKCFQAQKELIFIDPKNIQDALKWMAGNOLPSG
gi 14765710|TWLTAFLVKTFQAARAYIFIDEAHITQALWLSQOKDNG
gi 4557225 |TWLTAFLVKTFQAARAYIFIDEAHITQALWLSQOKDNG
gi 224053 |TWLTAFLVKTFQAARAYIFIDEAHITQALWLSQOKDNG
gi 6978425 |TWLTAFLVKTFQAARAYIFIDEAHITQALWLSQOKDNG
gi 2144118 |TWLTAFLVKTFQAARAYIFIDEAHITQALWLSQOKDNG
```

```
.....|.....|.....|.....|.....|.....|.....|.....|
1130      |1140      |1150      |1160
NOV2      |CYANVGNLLEITAMKGGVEDEVSLTAYVTAALLEMGKDVOD
gi 14765710|CFRSSGSLNNAIKGGVEDEVTLTAYITALLEPLTVTH
gi 4557225 |CFRSSGSLNNAIKGGVEDEVTLTAYITALLEPLTVTH
gi 224053 |CFRSSGSLNNAIKGGVEDEVTLTAYITALLEPLTVTH
gi 6978425 |CFRSSGSLNNAIKGGVEDEVTLTAYITALLEPLTVTH
gi 2144118 |CFRSSGSLNNAIKGGVEDEVTLTAYITALLEPLTVTH
```

```
.....|.....|.....|.....|.....|.....|.....|.....|
1170      |1180      |1190      |1200
NOV2      |PMVSOGLRCLNSATST-----LNTYTCALLAYIFSLAG
gi 14765710|PVVRNALFCLESARKTAEGDHGSHVYTKALLAYAFALAG
gi 4557225 |PVVRNALFCLESARKTAEGDHGSHVYTKALLAYAFALAG
gi 224053 |PVVRNALFCLESARKTAEGDHGSHVYTKALLAYAFALAG
gi 6978425 |PVVRNALFCLESARKTAEGDHGSHVYTKALLAYAFALAG
gi 2144118 |PVVRNALFCLESARKTAEGDHGSHVYTKALLAYAFALAG
```

```
.....|.....|.....|.....|.....|.....|.....|.....|
1210      |1220      |1230      |1240
NOV2      |EMDIRNIELKOLDQCAHISGESLYWSOKPTPSSNASPWSE
gi 14765710|NODKRKEVLKSLNEEAVKQDNSVHWERPQPKAPVGHYE
gi 4557225 |NODKRKEVLKSLNEEAVKQDNSVHWERPQPKAPVGHYE
gi 224053 |NODKRKEVLKSLNEEAVKQDNSVHWERPQPKAPVGHYE
gi 6978425 |NODKRKEVLKSLNEEAVKQDNSVHWERPQPKAPVGHYE
gi 2144118 |NODKRKEVLKSLNEEAVKQDNSVHWERPQPKAPVGHYE
```

```
.....|.....|.....|.....|.....|.....|.....|.....|
1250      |1260      |1270      |1280
NOV2      |PAA--VDELTAYALLAQLT-KPSLTOKETAKATSIVAWI
gi 14765710|PQAPSAEVEMTSYVLLAYLTAQAPPTSIEDLTSATNIVKWI
gi 4557225 |PQAPSAEVEMTSYVLLAYLTAQAPPTSIEDLTSATNIVKWI
gi 224053 |PQAPSAEVEMTSYVLLAYLTAQAPPTSIEDLTSATNIVKWI
gi 6978425 |PQAPSAEVEMTSYVLLAYLTAQAPPTSIEDLTSATNIVKWI
gi 2144118 |PQAPSAEVEMTSYVLLAYLTAQAPPTSIEDLTSATNIVKWI
```

```
.....|.....|.....|.....|.....|.....|.....|.....|
1290      |1300      |1310      |1320
```

Applicants: Guo
U.S.S.N.: 09/981,151

NOV2 AKQENAYGGFSSSTQDTVVALQALQKYATTAMPS-EEINZ
gi 14765710 | TKQONAOGGFSSSTQDTVVALHALSKYGAATFTRTGKAAQV
gi 4557225 | TKQONAOGGFSSSTQDTVVALHALSKYGAATFTRTGKAAQV
gi 224053 | TKQONAOGGFSSSTQDTVVALHALSKYGAATFTRTGKAAQV
gi 6978425 | TKQONS EGGFSSSTQDTVVALHALSKYGAATFTRTGKAAQV
gi 2144118 | TKQONS EGGFSSSTQDTVVALHALSKYGAATFTRTGKAAQV

1330 1340 1350 1360
NOV2 VIKSTENFQRTFNQSVNRLVFOQDELPMVPGMYTEASG
gi 14765710 | TIQSSGTFSSKFOVDNNRLLLOQVSLPTEPGYSLKVTG
gi 4557225 | TIQSSGTFSSKFOVDNNRLLLOQVSLPTEPGYSLKVTG
gi 224053 | TIQSSGTFSSKFOVDNNRLLLOQVSLPTEPGYSLKVTG
gi 6978425 | TIQSSGTFSSKFOVDNNRLLLOQVSLPTEPGYSLKVTG
gi 2144118 | TIQSSGTFSSKFOVDNNRLLLOQVSLPTEPGYSLKVTG

1370 1380 1390 1400
NOV2 EGCYVYQTVLRYNLPPTNMKTFSLSVLIGKARCEOPTSP
gi 14765710 | EGCYVYQTVLRYNLPPTNMKTFSLSVLIGKARCEOPTSP
gi 4557225 | EGCYVYQTVLRYNLPPTNMKTFSLSVLIGKARCEOPTSP
gi 224053 | EGCYVYQTVLRYNLPPTNMKTFSLSVLIGKARCEOPTSP
gi 6978425 | EGCYVYQTVLRYNLPPTNMKTFSLSVLIGKARCEOPTSP
gi 2144118 | EGCYVYQTVLRYNLPPTNMKTFSLSVLIGKARCEOPTSP

1410 1420 1430 1440
NOV2 RSLTETHTTSYVGSRSASNMAIVVKMISGFSPLMGTNOH
gi 14765710 | TSFQISLVSYTGSRSSNMAIVDKMVS GFIP LKPTVKM
gi 4557225 | TSFQISLVSYTGSRSSNMAIVDKMVS GFIP LKPTVKM
gi 224053 | TSFQISLVSYTGSRSSNMAIVDKMVS GFIP LKPTVKM
gi 6978425 | TSFQISLVSYTGSRSSNMAIVDKMVS GFIP LKPTVKM
gi 2144118 | TSFQISLVSYTGSRSSNMAIVDKMVS GFIP LKPTVKM

1450 1460 1470 1480
NOV2 LLLQPLVKVEFGDPTENIYLDELIKNTQYTFETISQSVL
gi 14765710 | LERSNHVSRTTEVSSNHVLIYLDKVSNOTLSLFFTVQDVP
gi 4557225 | LERSNHVSRTTEVSSNHVLIYLDKVSNOTLSLFFTVQDVP
gi 224053 | LERSNHVSRTTEVSSNHVLIYLDKVSNOTLSLFFTVQDVP
gi 6978425 | LERSNHVSRTTEVSSNHVLIYLDKVSNOTLSLFFTVQDVP
gi 2144118 | LERSNHVSRTTEVSSNHVLIYLDKVSNOTLSLFFTVQDVP

1490 1500 1510 1520
NOV2 VTNLKPAITIKVYDYVLPGSEKRSQYTIWVSMNDSIVDSV
gi 14765710 | VRDLKPAIVKVYDYETDEFAIAEYNAPCSKDLGNA----
gi 4557225 | VRDLKPAIVKVYDYETDEFAIAEYNAPCSKDLGNA----
gi 224053 | VRDLKPAIVKVYDYETDEFAIAEYNAPCSKDLGNA----
gi 6978425 | VRDLKPAIVKVYDYETDEFAIAEYNAPCSKDLGNA----
gi 2144118 | VRDLKPAIVKVYDYETDEFAIAEYNAPCSKDLGNA----

1530 1540
NOV2 ARHPEPPPPFKTEAFIPSLPGSVNN (SEQ ID NO:10)
gi 14765710 | ----- (SEQ ID NO:35)
gi 4557225 | ----- (SEQ ID NO:36)
gi 224053 | ----- (SEQ ID NO:37)
gi 6978425 | ----- (SEQ ID NO:38)
gi 2144118 | ----- (SEQ ID NO:39)

Pages 45, please replace Table 2E with the following

Table 2E Domain Analysis of NOV2

gnl|Pfam|pfam00207, A2M, Alpha-2-macroglobulin family. This family includes the C-terminal region of the alpha-2-macroglobulin family. (SEQ ID NO:80)
CD-Length = 751 residues, 98.5% aligned
Score = 563 bits (1451), Expect = 2e-161

Query: 728	EDSQVRQYFPETWLWDLFPIGNSGKEAVHVTVPDAITEWKAMSFCTSQSRGFGLSPTVGL	787
Sbjct: 4	DDITIRSYFPESWLWEVEEVDRSPVLTVNITLPDSITTWEILAVSLSNTKGLCVADPVEL	63
Query: 788	TAFKPFVVDLTLPSVVRGESFRLTATIFNYL-KDCIRVQTDLAKSHEYQLESWADSQTS	846
Sbjct: 64	TVFQDFFLELRPLPSVVRGEQVELRAVLNYLPSQDIKV-----VVQLEVEPLCQAG	115
Query: 847	SCLCADDKTHHWNITAVKLGHINFTISTKILDSNEPCGGQKGFVPQKGRSDTLIKPVLV	906
Sbjct: 116	FCSLATQTRSSQSVRPKSLSSVSFPVVVPLASGLSLVEVVASVPEFFVKDAVVKTLKV	175
Query: 907	KPEGVLVEKTHSSLLCP---KGGKVASESVSLELPVDIVPD-STKAYVTVLGDIMGTALQ	962
Sbjct: 176	EPEGARKEETVSSLLLPPEHLGGGLEVSEVPALKLPDDVPDTEAEAVISVQGDPAVAIQ	235
Query: 963	N-----LDGLVQMPSGCGEQNMVLFAPIIYVLQYLEKAGLLTE---EIRSRVAVGFLEIG	1013
Sbjct: 236	NTLSGEGLNLLRLPSGCGEQNMIIYMAPTVYVLHYLDETQWEKPGTKKKQKAIDLINKG	295
Query: 1014	YQKELMYKHSNGSYSAFGERDGNNGNTWLTAFVTKCFGQAQKFIFIDPKNIQDALKW-MAG	1072
Sbjct: 296	YQRQLNRYKADGSYAAFLHRA--SSTWLTAFVLKVFSQARNYVFIDEEHICGAVKWLILN	353
Query: 1073	NQLPSGCIYANVGNLLHTAMKGGVDD---EVSLTAYVTAALLEMGKDVDPMVSQGLRCL	1128
Sbjct: 354	QQKDDGVFRESGPVIHNEMKGGVGDDAEVEVTLTAFITIALLEAKLVCISPVVANALSIL	413
Query: 1129	KNSATSTTN-----LYTQALLAYIFSLAGEMDIRNILLKQLDQQAIIISGESIYWS--QK	1180
Sbjct: 414	KASDYLLNRYANGQRVYTLALTAYALALAGVLHKLKEILKSLKEELYKALVKGHWERPQK	473
Query: 1181	PTPSSNASPWSEPAAVDVELTAYALLAQLTQPSLTQKEIAKATSIVAWLAKQHNAYGGFS	1240
Sbjct: 474	PKDAPGHPYSPQPQAAAVEMTSYALLALT--LLPFPKVEMAPKVVKWLTEQQYYGGGFG	531
Query: 1241	STQDTVVALQALAKYATTAYMPSE-EINLVVKSTEN-FORTFNIQSVNRLVFQQDTLP-N	1297
Sbjct: 532	STQDTVMALQALSKYGIATPTHKEKNLSVTIQSPSGSFKSHFQILNNAFLLRPVELPLN	591
Query: 1298	VPGMYTLEASGQGCYVQTVLRYNLPPTNMKTFSLSVEIGKARCEQPTSPR-SLTLTIH	1356
Sbjct: 592	EGFTVTAKVTGQGTLLTVTTYRYKVLDDKNTFCFDLKIETVPDTCVEPKGAKNSDYLISIC	651
Query: 1357	TSYVGSRSSNMAIVEVKMLSGFSPMEGT--NQLLLQQPLVKKVEFGTDTLNIYLDDELIX	1414
Sbjct: 652	TRYAGSRSDSGMAIADISMLTGFIPLKPDLLKLENGVDRYVSKYEIDGNHVLLYLDKVVSH	711
Query: 1415	-NTQTYTFTISQSVLVTNLKPATIKVYDYLP 1445 (of SEQ ID NO:10)	

Applicants: Guo
U.S.S.N.: 09/981,151

Sbjct: 712 SETECVGFKIHQDFEVGLLPASVKVYDYYP 743 (SEQ ID NO:80)

Pages 46, please replace Table 2F with the following:

Table 2F Domain Analysis of NOV2

gal|Pfam|pfam01835, A2M_N, Alpha-2-macroglobulin family N-terminal region. This family includes the N-terminal region of the alpha-2-macroglobulin family. (SEQ ID NO:81)
CD-Length = 620 residues, 98.4% aligned
Score = 236 bits (603), Expect = 5e-63

```
Query: 5      LLLGMLALSPAIAEEL--PNYLVTLPARLNFPSVQKVCLDLSPGYSDVKFTVTLETDKDT 62
           || +| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 2      LLWLLLLLLLLFFDSSLQPRYMVIVPSILRTETPEKVCVQLHDLNETVTVTVSLHSFPGK 61

Query: 63     QKLLEYSGLK---KRHLHCISFLVPPPA---GGTEEVATIRVSGVGNNISFEEKKKVLIQ 116
           + | + | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 62     RNLSSLFTVLLSSKDLFHCVSFTVPQGLFKSSKGEESFVVVQVKGPTHTFKEKVTVLVS 121

Query: 117    RQNGNFTFVQTDKPLYTPGQQVYFRIVTMSNFVPVNDKYSMVELQDPNSNRIAQWLEVVP 176
           + | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 122    SRRGLVFIQTDKPIYTPGQTVRYRVFSVDENLRPLNELI-LVYIEDPEGNRVDQWEVNKL 180

Query: 177    EQGIVDLFSFLAPEAMLGTYTVAV---AEGKTFGT--FSVEEYVLSPFLLLLSSVLPKFK 231
           | | | | | | + | + | | + + + + + + | | | | | | | | | | |
Sbjct: 181    EGGIFQLSFPIPISEPIQGTWKIVARYESGPESNYTHYFEVKEY-----VLPSFEVS 231

Query: 232    VEVVEPKELSTVQESFLVKICCRYTYGKPMLGAVQVSVQKANTYWYREVEREQLPDKCR 291
           + + | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 232    ITPPKPFIYYDNFKEFEVETICARYTYGKVPVGVAYVRFGVK-----DEDGKKELLAGLE 285

Query: 292    NLSGQTDKTG--CFSAPVDMATFDLIGYAY-SHQINIVATVVEEGTGVEANA-TQNIYIS 347
           + | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 286    ERAKLLDGNGEICLSQEVLLKELQLKNEDLEGKSLYVAVAVIESEGGDMEEAELGGIKIV 345

Query: 348    PQMGSMFTEDTSNFIYHPNFFPSGKMLLKFPQGGVLPCKNHLVFLVIYGTNGTFNQTLVTD 407
           + | | | + + | | | | | | | | | | | | | | | | | | | | |
Sbjct: 346    RSPYKLFVKTPSHFKPGIPFFLKVLVDPDGS--PAPNVPVK--VSAQDASYYSNGTTD 401

Query: 408    NNGLAPFTLETSGWNGTDVSLEGKFQMEDLVYNPEQVPRYYQNAYLHLRPFYSTTRSFLG 467
           + | | | | ++ | | | | + + | + + + + + | | | | | | | | |
Sbjct: 402    EDGLAQFSINTS--GISSLSITVRTNHKELPEEVQAHAEAQATAYSTVSL--SKSYIHLS 457

Query: 468    IHRNLGPLKCGQPQEVLDVYYIDPADASPDQEISFSYYLIGKSLVMEGQKHLNSKKKGL 527
           | | | | | | | | | | | | | | | | | | | | | | | | | | |
Sbjct: 458    IER---TLPCGPGVGEQANFILRGKSLGELKILHFYYLIMSKGKIVKTGRE---PREPG 510

Query: 528    KASFSLSLTFTSRLAPDPSLVIYAIFPSGGVVADKIQFSVEMCFDN-----QQL 576
           + | | | | + | | | | | | | | | | | | | | | | | | | | |
Sbjct: 511    QGLFSLSIPVTPDLAPSFRVLVAYYILPQGEVVADSVWIDVEDCCANKLDLSFSPSKDYRL 570

Query: 577    PGAEVELQLQAAPGSLCALRAVDESIVLLRPDRELSNRSVY 617 (of SEQ ID NO:10)
           | + | + | + + | | | | | | | | | | | | | | | | | | | |
Sbjct: 571    PAQQVKLRVEADPQSLVALRAVDQAVYLLKPKAKLSMSKVY 611 (SEQ ID NO:81)
```

Applicants: Guo
U.S.S.N.: 09/981,151

At page 52 please replace Table 3E with the following:

Table 3E. BLAST results for NOV3					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
<u>gi 12858115 dbj BAB31203.1 AK018423 BAB31203</u>	putative [Mus musculus]	373	187/310 (60%)	226/310 (72%)	6e-87
<u>gi 3024224 sp Q28727 NTCI_RABIT NP 058918</u>	ILEAL SODIUM/BILE ACID COTRANSPORTER (ILEAL NA(+)/BILE ACID COTRANSPORTER) (NA+ DEPENDENT ILEAL BILE ACID TRANSPORTER) (ILEAL SODIUM- DEPENDENT BILE ACID TRANSPORTER) (ISBT) (SODIUM/TAURO CHOLATE COTRANSPORTIN G POLYPEPTIDE, ILEAL)	347	116/279 (41%)	173/279 (61%)	1e-52
<u>gi 8394281 ref NP_050918.1 NP 035518</u>	solute carrier family 10, member 2 [Rattus norvegicus]	348	130/344 (37%)	195/344 (55%)	2e-52
<u>gi 6755530 ref NP_035518.1 NP 35518</u>	solute carrier family 10, member 2 [Mus musculus]	348	125/313 (39%)	191/313 (60%)	4e-52
<u>gi 6755530 ref NP_035518.1 NP 35518</u>	solute carrier family 10, member 2 [Mus musculus]	348	125/313 (39%)	191/313 (60%)	4e-52

Applicants:
U.S.S.N.:

<u>qi</u> <u>2842631</u> <u>sp</u> <u>Q6041</u> <u>4</u> <u>NTCI</u> <u>CRIGR</u> <u>Q60414</u>	ILEAL SODIUM/BILE ACID COTRANSPORTER (ILEAL NA(+)/BILE ACID COTRANSPORTER) (NA+ DEPENDENT ILEAL BILE ACID TRANSPORTER) (ILEAL SODIUM- DEPENDENT BILE ACID TRANSPORTER) (ISBT) (SODIUM/TAURO CHOLATE COTRANSPORTIN G POLYPEPTIDE, ILEAL)	348	121/306 (39%)	185/306 (59%)	4e-52
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At page 53 please replace Table 3F with the following:

Table 3F. ClustalW Analysis of NOV3

- 1) NOV3 (SEQ ID NO:12)
 3) gi|12858115|dbj|BAB31203.1| gi|12858115| BAB31203 (AK018423) putative [Mus musculus] (SEQ ID NO:40)
 4) gi|3024224|sp|Q28727|NTCI-RABIT gi|3024224| NP058918 ILEAL SODIUM/BILE ACID COTRANSPORTER (ILEAL NA(+)/BILE ACID COTRANSPORTER) (NA+ DEPENDENT ILEAL BILE ACID TRANSPORTER) (ILEAL SODIUM-DEPENDENT BILE ACID TRANSPORTER) (ISBT) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE, ILEAL) (SEQ ID NO:41)
 5) gi|8394281|ref|NP_058918.1| gi|8394281| NP035518 solute carrier family 10, member 2 [Rattus norvegicus] (SEQ ID NO:42)
 6) gi|6755530|ref|NP_035518.1| gi|6755530| NP035518 solute carrier family 10, member 2 [Mus musculus] (SEQ ID NO:43)
 7) gi|6755530|ref|NP_035518.1| gi|6755530| NP035518 solute carrier family 10, member 2 [Mus musculus] (SEQ ID NO:44)
 8) gi|2842631|sp|Q60414|NTCI-CRICK gi|2842631| Q60414 ILEAL SODIUM/BILE ACID COTRANSPORTER (ILEAL NA(+)/BILE ACID COTRANSPORTER) (NA+ DEPENDENT ILEAL BILE ACID TRANSPORTER) (ILEAL SODIUM-DEPENDENT BILE ACID TRANSPORTER) (ISBT) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE, ILEAL) (SEQ ID NO:45)

NOV3
 g1 | 12858115 | MRANCS-S~~SS~~SACPANSS~~EE~~EE~~EP~~VGLEVG~~GN~~TE~~LV~~FTV~~ST~~
 g1 | 3024224 | MSTDCV-GNSTCPVNST~~ED~~PPVGM~~EG~~HAN~~KK~~LF~~FT~~V~~ESA~~
 g1 | 8394281 | MSNLTVCGLANATVCEGASCVAPESNFNAILSV~~VT~~STVLT
 g1 | 6755530 | MDN~~SSV~~-C~~SP~~PNATVCEG~~SC~~SV~~TS~~ESNFNAILSV~~VT~~STVLT
 g1 | 2842631 | MDN~~SSV~~-C~~PN~~PNATVCEG~~SC~~SV~~TS~~ESNFNAILSV~~VT~~STVLT

NOV3
 g1 | 12858115 | L~~NG~~LV~~MF~~SG~~CS~~SV~~EE~~ER~~KL~~WSH~~IR~~RPWGIAV~~GL~~LCQ~~FG~~GM
 L~~NG~~LV~~MF~~SG~~CS~~SV~~EE~~ER~~KL~~WSH~~IR~~RPWGIAV~~GL~~LCQ~~FG~~GM

Applicants: Guo
U.S.S.N.: 09/981,151

```
gi|3024224| ILLALVMFMSGCNVEHKKFLGHIRRPWGIIVGFLCQFGIM
gi|8394281| ILLALVMFMSGCNVEHKKFLGHIRRPWGIIVGFLCQFGIM
gi|6755530| ILLALVMFMSGCNVEHKKFLGHIRRPWGIIVGFLCQFGIM
gi|2842631| ILLALVMFMSGCNVEHKKFLGHIRRPWGIIVGFLCQFGIM
```

```
          90      100      110      120
NOV3      PFTATLALATGFSIRKPVQAAVLIMGCCRG---APSLTSP
gi|12858115| PLTATLALATGFGIKPFOAAVLIMGCCPGGTISNVLTVWV
gi|3024224| PLTGFMLSVAFGIEIPVQAVVVLIMGCCPGGTASNILAYWV
gi|8394281| PLTGFMLSVAFGIEIPVQAVVVLIMGCCPGGTASNILAYWV
gi|6755530| PLTGFMLSVAFGIEIPVQAVVVLIMGCCPGGTASNILAYWV
gi|2842631| PLTGFMLSVAFGIEIPVQAVVVLIMGCCPGGTASNILAYWV
```

```
          130      140      150      160
NOV3      SGLMRTWISG-----ALGMMPLCLVYVWSWSLQONT
gi|12858115| DGDMDLSISMTTCSTVAALGMMPLCLVYVWSLTONLV
gi|3024224| DGDMDLSVSMITCSTLLALGMMPLCLVYTKMWVDSGTIV
gi|8394281| DGDMDLSVSMITCSTLLALGMMPLCLVYTKMWVDSGTIV
gi|6755530| DGDMDLSVSMITCSTLLALGMMPLCLVYTKMWVDSGTIV
gi|2842631| DGDMDLSVSMITCSTLLALGMMPLCLVYTKMWVDSGTIV
```

```
          170      180      190      200
NOV3      IPYONIGLSIGITLVCLTIPVAFGVAVNTPKOSKIILK
gi|12858115| IPYQ----SIGITLVSLVPEVASGVYVNHKWPQKATVILK
gi|3024224| IPYD----NIGTSLVALVPEVSIGMVVNHKWPQKAKIILK
gi|8394281| IPYD----SIGISLVALVIPVSIGMVVNHKWPQKAKIILK
gi|6755530| IPYD----SIGISLVALVIPVSIGMVVNHKWPQKAKIILK
gi|2842631| IPYD----SIGTSLVALVPEVSIGMVVNHKWPQKAKIILK
```

```
          210      220      230      240
NOV3      --AVVGGVLELVAVAGVVLARGSWNSDITLTISFIFFP
gi|12858115| VGAILGGMLELVAVTCAVLAKG-WNTEVTLVLVISCIFP
gi|3024224| VGSIAGALLIVLIAVVGGLYQSAWIEPKLWIIGTIFP
gi|8394281| VGSIAGALLIVLIAVVGGLYQSAWIEPKLWIIGTIFP
gi|6755530| VGSITGVLLIVLIAVVGGLYQSAWIEPKLWIIGTIFP
gi|2842631| VGSIAGALLIVLIAVVGGLYQSAWIEPKLWIIGTIFP
```

```
          250      260      270      280
NOV3      IGVVTGFLALFTHOSQ--RTIPFLGLAFKTPCDTILA
gi|12858115| VGVVTGFLALFTHOSWRCRTISLETGAONIOLCIAMTQ
gi|3024224| AGYSLGFFLARAGQPWYRCRTVALETGONTOLCSTIVO
gi|8394281| AGYSLGFFLARAGQPWYRCRTVALETGONTOLCSTIVO
gi|6755530| AGYSLGFFLARAGQPWYRCRTVALETGONTOLCSTIVO
gi|2842631| AGYGLGFFLARAGQPWYRCRTVALETGONTOLCSTIVO
```

```
          290      300      310      320
NOV3      MHSCEPSRLIYAFIPLLYGTFQIEDGFIIVEE-----
gi|12858115| LSFSAEYLVQLLNEA-LAYGLFQVHGLLVAAYQAYKRR
gi|3024224| LSFSPEDLYVFTFP-LIYSTFQAFAAELGIYVAYKRC
gi|8394281| LSFSPEDLNLVFTFP-LIYVVFQVFAAILGMYVYKRC
gi|6755530| LSFSPEDLNLVFTFP-LIYVVFQVFAAVILGIYVYKRC
gi|2842631| LSFSPEDLNLVFTFP-LIYSTFQAFAAELGAYVAYKRC
```

```
          330      340      350      360
NOV3      -----RTEDTEC-----DGSP--LPEVFT-----EVTIIP
gi|12858115| QKSKCRRHPCPDVCYKQPRETSALFKGDEAAVTLGP
gi|3024224| HG-KNDAEFPDIKDT--KTEP--ESSFEQ-----MNGG
```

Applicants: Guo
U.S.S.N.: 09/981,151

```
gi|8394281|      HG-KNDAEFLKTDN--DMDP--MPSFOE-----TNKG
gi|6755530|      YG-KNDAEFLKTDN--EMDS--RPSFDE-----TNKG
gi|2842631|      HG-KNNTLQEKTDN--EMEP--RSSFOE-----TNKG
```

```

              370      380
NOV3          .....|.....|.....|
gi|12858115|  KOPRI----- (SEQ ID NO:12)
gi|3024224|  VQPEQHHRAAELTSHIPSC (SEQ ID NO:40)
gi|8394281|  FQPE----- (SEQ ID NO:41)
gi|6755530|  FQPDEK----- (SEQ ID NO:42)
gi|2842631|  FQPDEK----- (SEQ ID NO:43)
              FQPDEK----- (SEQ ID NO:45)
```

Page 55, please replace Table 3G with the following

Table 3G Domain Analysis of NOV3

gnl|Pfam|pfam01758, SBF, Sodium Bile acid symporter family. This family consists of Na+/bile acid co-transporters. These transmembrane proteins function in the liver in the uptake of bile acids from portal blood plasma a process mediated by the co-transport of Na+. Also in the family is ARC3 from *S. cerevisiae* this is a putative transmembrane protein involved in resistance to arsenic compounds. (SEQ ID NO:82)
CD-Length = 186 residues, 80.1% aligned
Score = 75.9 bits (185), Expect = 3e-15

```

Query: 39  TIMMGLLMFSLGCSVEIRKLWSHIRRPWGIAVGLLCQFGLMPFTAYLLAIS-FSLKPVQA 97
          + + | + | | + | | | + | | | + + | | | | |
Sbjct: 1   ALGLFLMMFSMGLKVRFEDLKEALRRPKALILGLLLQWIIMPLLMFILAWLLLRPPELA 60

Query: 98  IAVLIMGCCRG---APSLTFSPSGLMEIWIS-----GALGMMPLCIYLTWSWSLQQN 147
          + + + + | | + | + | + + + + | + | | + |
Sbjct: 61  TGLILVGCAPGGAMSNVWTYLAKGDVELSVVMVALSTLLAPLVTPLLSFLLAGLL----- 115

Query: 148 LTIPYQNIGLSLGITLVCLTIPVAFGVVNYRWP 181 (of SEQ ID NO:12)
          + + + + | + | | + | + | |
Sbjct: 116 VHVDAVSPWSLIKSVLVYVIPLIAGMLTRYFLP 149 (SEQ ID NO 82)
```

At page 61, please replace Table 4C with the following:

Table 4C. BLAST results for NOV4

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 4505773 ref NP_002625.1 NP 002625	prohibitin [Homo sapiens]	272	236/270 (87%)	251/270 (92%)	e-123
gi 92643 pir A39682	prohibitin - rat	272	235/270 (87%)	251/270 (92%)	e-123

Applicants: Guo
U.S.S.N.: 09/981,151

<u>gi 7298546 gb AAF53765.1 </u> (AE003661) <u>AAF53765</u>	1(2)37Cc gene product [Drosophila melanogaster]	276	178/270 (65%)	220/270 (80%)	8e-96
<u>gi 2055454 gb AAB53231.1 </u> (U97204) <u>AAB53231</u>	prohibitin-like molecule TC-PRO-1 [Toxocara canis]	274	153/264 (57%)	209/264 (78%)	9e-80
<u>gi 13491275 gb AAK27865.1 </u> (AC087079) <u>AAK27865</u>	Hypothetical protein Y37E3.9 [Caenorhabditis elegans]	275	154/270 (57%)	210/270 (77%)	6e-79

At page 61 please replace Table 4D with the following:

Table 4D ClustalW Analysis of NOV4

- 1) NOV4 (SEQ ID NO:14)
- 2) gi|4505773|ref|NP_002625.1| NP 002625 gi|4505773| prohibitin [Homo sapiens] (SEQ ID NO:46)
- 3) gi|92643|pir|A39682 A39682 gi|6679299| prohibitin - rat (SEQ ID NO:47)
- 4) gi|7298546|gb|AAF53765.1| AAF53765 (AE003661) gi|7298546| 1(2)37Cc gene product [Drosophila melanogaster] (SEQ ID NO:48)
- 5) gi|2055454|gb|AAB53231.1| AAB53231 (U97204) gi|2055454| prohibitin-like molecule TC-PRO-1 [Toxocara canis] (SEQ ID NO:49)
- 6) gi|13491275|gb|AAK27865.1| AAK27865 (AC087079) gi|13491275| Hypothetical protein Y37E3.9 [Caenorhabditis elegans] (SEQ ID NO:50)

		10	20	30	40
NOV4		---MAAKVF	EFIGK	FGLALV	VAGGVNSALYSVDAGHRAV
gi 4505773		---MAAKVF	ESIGK	FGLALV	VAGGVNSALYNVDAGHRAV
gi 6679299		---MAAKVF	ESIGK	FGLALV	VAGGVNSALYNVDAGHRAV
gi 7298546		---MAAQFN	RIGOMGL	GVAVLGGV	NNSALYNVEGGHRAV
gi 2055454		-MAGAQK	ELGRIG	IGVALAVIT	GGVNSALYNVDGGORAV
gi 13491275		MAASAQK	ELGRIG	TVGVGLST	AGGTAQALYNVDGGORAV

		50	60	70	80
NOV4		VFDRFR	GVQDI	VVGEGTH	FLIPWQKSIIFDCRS
gi 4505773		IFDRFR	GVQDI	VVGEGTH	FLIPWQKPIIFDCRS
gi 6679299		IFDRFR	GVQDI	VVGEGTH	FLIPWQKPIIFDCRS
gi 7298546		IFDRFT	GVQDI	VVGEGTH	FLIPWQKPIIFDIRS
gi 2055454		IFDRFT	GVQDI	VVGEGTH	FLIPWQKPIIFDIRS
gi 13491275		IFDRFS	GVQDI	VVGEGTH	FLIPWQKPIIFDIRS

		90	100	110	120
NOV4		VITGSK	DLQNVN	ITLRIL	RPVASQLPRI
gi 4505773		VITGSK	DLQNVN	ITLRIL	RPVASQLPRI
gi 6679299		VITGSK	DLQNVN	ITLRIL	RPVASQLPRI
gi 7298546		VITGSK	DLQNVN	ITLRIL	RPVASQLPRI
gi 2055454		TITGSK	DLQNVN	ITLRIL	RPVASQLPRI
gi 13491275		TITGSK	DLQNVN	ITLRIL	RPVASQLPRI

		130	140	150	160
NOV4		VPPSIT	NEVLK	SVVAF	FDAGELITORE
gi 4505773		VLPSIT	NEVLK	SVVAF	FDAGELITORE
gi 6679299		VLPSIT	NEVLK	SVVAF	FDAGELITORE
gi 7298546		VLPSIT	NEVLK	SVVAF	FDAGELITORE
gi 2055454		VLPSIT	NEVLK	SVVAF	FDAGELITORE
gi 13491275		VLPSIT	NEVLK	SVVAF	FDAGELITORE

Applicants: Guo
U.S.S.N.: 09/981,151

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      170      180      190      200
      . . . . .
NOV4  AATFGLILDDVSLTYLTFTGKEFTTEAVEAKQIAQQEAEERAR
gi | 4505773 | AATFGLILDDVSLTHLTFTGKEFTTEAVEAKQIAQQEAEERAR
gi | 6679299 | AATFGLILDDVSLTHLTFTGKEFTTEAVEAKQIAQQEAEERAR
gi | 7298546 | AKQFGFILDVSLTHLTFTGKEFTTEAVEAKQIAQQEAEERAR
gi | 2055454 | ARQFGFILDVSLTHLTFTGKEFTTEAVEAKQIAQQEAEERAR
gi | 13491275 | AATFGLILDDVSLTHLTFTGKEFTTEAVEAKQIAQQEAEERAR

      210      220      230      240
      . . . . .
NOV4  FVVEKAEQKKAAALISAEGDSKVAELFTNSLATAGDALIE
gi | 4505773 | FVVEKAEQKKAAALISAEGDSKVAELFTNSLATAGDGLIE
gi | 6679299 | FVVEKAEQKKAAALISAEGDSKVAELFTNSLATAGDGLIE
gi | 7298546 | FVVEKAEQKKAAALISAEGDSKVAELFTNSLATAGDGLIE
gi | 2055454 | FVVEKAEQKKAAALISAEGDSKVAELFTNSLATAGDGLIE
gi | 13491275 | FVVEKAEQKKAAALISAEGDSKVAELFTNSLATAGDGLIE

      250      260      270
      . . . . .
NOV4  LRKLEAVEDIAYQLLSRNTTYLRAGOSMPLOLRW---- (SEQ ID NO:14)
gi | 4505773 | LRKLEAAEDIAYQLLSRNTTYLRAGOSVLLQLPQ---- (SEQ ID NO:46)
gi | 6679299 | LRKLEAAEDIAYQLLSRNTTYLRAGOSVLLQLPQ---- (SEQ ID NO:47)
gi | 7298546 | LRKLEAAEDIAYQLLSRSGVAYLPSGOSTHNLPSITIAQ (SEQ ID NO:48)
gi | 2055454 | LRKLEAAEETAEERMSKTRNVLYLPGNQNTLENLPA---- (SEQ ID NO:49)
gi | 13491275 | LRKLEAAEETAEERMAKNKNTVLYLPGNQNTLENLQS---- (SEQ ID NO:50)

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At page 62 please replace Table 4E with the following:

Table 4E. Domain Analysis of NOV4

gi | Pfam | pfam01145, Band 7, SPFH domain / Band 7 family. This family also includes proteins with high blast scores to known Band 7 protein: HflC from E. coli HflK from E. coli, and Prohibitin family members (SEQ ID NO:83)
CD-Length = 191 residues, 91.6% aligned
Score = 157 bits (397), Expect = 7e-40

```

Query:  28  YSV DAGHRA VV FDR FRGVQDIVVGK GTHCLIPWLQKSIIFDCRSQPRNV PVITGSKDLQN 87
      |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Sbjct:  17  KIVKEYERG VIFRLGRYVRQ-VVGPGLHFIIPFIDTVKKVDLRTTVVYDVPSQEIIITKDNV 75

Query:  88  VNLTLRIIFRPVASQLPHIFTSSGEDHDERVPPSITNKILKSVVARFEAGELITQREQIS 147
      |  +  +++  |  |  ++  |  |  |  |  |  +  |  ++  +  +  |  ++  +  +  +
Sbjct:  76  VVIVDAVVYR VVDPLKAVYEVED---AERALPQLAQTTLRNVIGQFTLDEILTERERIN 132

Query:  148  RQVSDDLTEPAATFGLILDDVSLTYLTFTGKEFTTEAVEAKQIAQQEAEERARFVVEKAEQKK 207
      |  +  +  |  |  +  +  +  +  +  +  |  +  |  +  |  ++  |  |  +  +  +  |  +
Sbjct:  133  SQLREILDEATDPWGIKVERVEIKDIRLP EEVQRAMAAQMEAAREA-RAKILEAEGEQEA 191

Query: (aa 28-207 of SEQ ID NO:14)
Sbjct: (SEQ ID NO:83)

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Applicants: Guo
U.S.S.N.: 09/981,151

At page 63, please replace Table 4F with the following:

Table 4F. Domain Analysis of NOV4	
gnl Smart smart00244,	PHB, prohibitin homologues; prohibitin homologues (SEQ ID NO:84)
CD-Length = 160 residues, 98.8% aligned	
Score = 97.4 bits (241), Expect = 9e-22	

Query: 28 YSVDAGHRAVVFDRFRGVQDIVVGKGTHCLIPWLQKSIIFDCRSQPRNVPVITG-SKDLQ 86
+ | | | + | | | + | | | + | + | | | + | | + | |
Sbjct: 3 FYVIGEGERGTVVERLGRVLK-VLGPGLHFVIPFIDDKRVLDLRAQTDDVPPQEVITKDNV 61

Query: 87 NVNLTLRRIIFRPVASQLPHIFTSSGEDHDERVPPSITNKILKSVMARFEAGELIT-QREQ 145
|++ + + | | | ++ | | | + | + | + + | + | + | +
Sbjct: 62 TVSVDAVVYYR-VLDPLKAVYGV--LDADYRALRQLAQTTLRSVIGKRTLDELLTDEREK 118

Query: 146 ISRQVSDDLTEPAATFGLILDDVSLTYLTFGKEFIEAVEAKQ 187 (of SEQ ID NO:14)
| | + ++ | | | + | + ++ | | + + + | | + | + |
Sbjct: 119 ISENIREELNEAAEPWGIEVEDVEIKDIRLP EEIKEAMEAQ 160 (SEQ ID NO:84)

At page 67 please replace Table 5C with the following:

Table 5C. BLAST results for NOV5					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
<u>gi 15294659 ref XP_054070.1 </u> XP 05407	macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens]	711	561/720 (77%)	577/720 (79%)	0.0
<u>gi 10337615 ref NP_066278.1 </u> NP 066278	macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens]	711	560/720 (77%)	576/720 (79%)	0.0
<u>gi 123114 sp P26927 </u> HCFL HUMAN-P26927	HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (MACROPHAGE STIMULATORY PROTEIN) (MSP) (MACROPHAGE STIMULATING PROTEIN)	711	560/720 (77%)	576/720 (79%)	0.0
<u>gi 15299258 ref XP_017811.2 </u> XP 017811	hypothetical protein XP_017811 [Homo sapiens]	529	440/532 (82%)	456/532 (85%)	0.0
<u>gi 90615 pir A40332</u> A40332	macrophage-stimulating protein 1 precursor - mouse	716	449/725 (61%)	507/725 (69%)	0.0

Applicants: Guo
U.S.S.N.: 09/981,151

At page 68 please replace Table 5D with the following:

Table 5D Clustal W Sequence Alignment

- 1) NOV5 (SEQ ID NO:16)
- 2) gi|15294659|ref|XP_054070.1| gi|15294659| XP 05407 macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens] (SEQ ID NO:51)
- 3) gi|10337615|ref|NP_066278.1| gi|10337615| NP 066278 macrophage stimulating 1 (hepatocyte growth factor-like) [Homo sapiens] (SEQ ID NO:52)
- 4) gi|123114|sp|P26927|HGFL_HUMAN gi|123114| P26927HEPATOCYTE GROWTH FACTOR-LIKE PROTEIN PRECURSOR (MACROPHAGE STIMULATORY PROTEIN) (MSP) (MACROPHAGE STIMULATING PROTEIN) (SEQ ID NO:53)
- 5) gi|15299258|ref|XP_017811.2| gi|15299258| XP 017811hypothetical protein XP_017811 [Homo sapiens] (SEQ ID NO:54)
- 6) gi|90615|pir|A40332 gi|90615| A40332 macrophage-stimulating protein 1 precursor - mouse (SEQ ID NO:55)

```

      10      20      30      40
NOV5      ....|....|....|....|....|....|....|....|
gi|15294659| MGWLPLLLLLTQCLGVPGQRSPLNDFQVLRGTELOHLLHA
gi|10337615| MGWLPLLLLLTQCLGVPGQRSPLNDFQVLRGTELOHLLHA
gi|123114|   MGWLPLLLLLTQCLGVPGQRSPLNDFQVLRGTELOHLLHA
gi|15299258| MGWLPLLLLLTQCLGVPGQRSPLNDFQVLRGTELOHLLHA
gi|90615|    MGWLPLLLLLVQCSRALGQRSPLNDFQVLRGTELRNLLLT
```

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      50      60      70      80
NOV5      VVPGPWQEDVADAEECAGRCGPLMDCRAFHYNVSSHGCQL
gi|15294659| VVPGPWQEDVADAEECAGRCGPLMDCRAFHYNVSSHGCQL
gi|10337615| VVPGPWQEDVADAEECAGRCGPLMDCRAFHYNVSSHGCQL
gi|123114|   VVPGPWQEDVADAEECAGRCGPLMDCRAFHYNVSSHGCQL
gi|15299258| -----MDCRAFHYNVSSHGCQL
gi|90615|    AVPGPWQEDVADAEECARRCGPLMDCRAFHYNVSSHGCQL
```

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      90     100     110     120
NOV5      LPWTOHSPHTRLRRSGRCDLFQKKDYVRTCIMNNGVGVRG
gi|15294659| LPWTOHSPHTRLRRSGRCDLFQKKDYVRTCIMNNGVGVRG
gi|10337615| LPWTOHSPHTRLRRSGRCDLFQKKDYVRTCIMNNGVGVRG
gi|123114|   LPWTOHSPHTRLRRSGRCDLFQKKDYVRTCIMNNGVGVRG
gi|15299258| LPWTOHSPHTRLRRSGRCDLFQKKDYVRTCIMNNGVGVRG
gi|90615|    LPWTOHSPHTRLRRSGRCDLFQKKDYVRTCIMNNGVGVRG
```

```

      130     140     150     160
NOV5      TMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNP
gi|15294659| TMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNP
gi|10337615| TMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNP
gi|123114|   TMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNP
gi|15299258| TMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNP
gi|90615|    TMATTVGGLPCQAWSHKFPNDHKYTPTLRNGLEENFCRNP
```

```

      170     180     190     200
NOV5      DGDPPGWPWCYTTPDAVRFQSCGIKSCREAAACVWCNGEYR
gi|15294659| DGDPPGWPWCYTTPDAVRFQSCGIKSCREAAACVWCNGEYR
gi|10337615| DGDPPGWPWCYTTPDAVRFQSCGIKSCREAAACVWCNGEYR
gi|123114|   DGDPPGWPWCYTTPDAVRFQSCGIKSCREAAACVWCNGEYR
gi|15299258| DGDPPGWPWCYTTPDAVRFQSCGIKSCREAAACVWCNGEYR
gi|90615|    DGDPPGWPWCYTTPDAVRFQSCGIKSCREAAACVWCNGEYR
```

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      210     220     230     240
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Applicants: Guo
U.S.S.N.: 09/981,151

NOV5
gi | 15294659 | GAVDRTESGRECORWDLQHPHQHPFEPGKFLDOGLDDNYC
gi | 10337615 | GAVDRTESGRECORWDLQHPHQHPFEPGKFLDOGLDDNYC
gi | 123114 | GAVDRTESGRECORWDLQHPHQHPFEPGKFLDOGLDDNYC
gi | 15299258 | GAVDRTESGRECORWDLQHPHQHPFEPGKFLDOGLDDNYC
gi | 90615 | GEVDVTESGRECORWDLQHPHSHFPQEPKFLDKLDLDNYC

250 260 270 280
NOV5
gi | 15294659 | RNPDGSERPWCYTTDPQIEREFCDLPRCG-----SE
gi | 10337615 | RNPDGSERPWCYTTDPQIEREFCDLPRCG-----SE
gi | 123114 | RNPDGSERPWCYTTDPQIEREFCDLPRCG-----SE
gi | 15299258 | RNPDGSERPWCYTTDPQIEREFCDLPRCG-----SE
gi | 90615 | RNPDGSERPWCYTTDPNVEREFCDLPSCEPNLPPTVKGSK

290 300 310 320
NOV5
gi | 15294659 | AOPRQEAATVSCFRGKGEGYRGTTANTTTAGVPCORWDAOI
gi | 10337615 | AOPRQEAATVSCFRGKGEGYRGTTANTTTAGVPCORWDAOI
gi | 123114 | AOPRQEAATVSCFRGKGEGYRGTTANTTTAGVPCORWDAOI
gi | 15299258 | AOPRQEAATVSCFRGKGEGYRGTTANTTTAGVPCORWDAOI
gi | 90615 | SQRRNKGAKSCFRGKGEGYRGTTNTTSGVPCORWDAOS

330 340 350 360
NOV5
gi | 15294659 | PHQHRFTPEKYACKDLRENF CRNPDGSEAPWCFTLRPGMR
gi | 10337615 | PHQHRFTPEKYACKDLRENF CRNPDGSEAPWCFTLRPGMR
gi | 123114 | PHQHRFTPEKYACKDLRENF CRNPDGSEAPWCFTLRPGMR
gi | 15299258 | PHQHRFTPEKYACKDLRENF CRNPDGSEAPWCFTLRPGMR
gi | 90615 | PHQHRFTPEKYACKDLRENF CRNPDGSEAPWCFTSRPGMR

370 380 390 400
NOV5
gi | 15294659 | AAFYQIIRCTDDVRPQTATTAQGSSTAARSAPPAVSSA
gi | 10337615 | AAFYQIIRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVOG
gi | 123114 | AAFYQIIRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVOG
gi | 15299258 | VGEYQIIRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVOG
gi | 90615 | MAFCEQIIRCTDDVRPQDCYHGAGEQYRGTVSKTRKGVOG

410 420 430 440
NOV5
gi | 15294659 | SAGPLRRRTSRSSRLPPNRMHNWRTSAGTOMGIA MGPGA
gi | 10337615 | QRWSAETPHKPQFTFTSEPHAQLEENFCRNPDGDSHGP--
gi | 123114 | QRWSAETPHKPQFTFTSEPHAQLEENFCRNPDGDSHGP--
gi | 15299258 | QRWSAETPHKPQFTFTSEPHAQLEENFCRNPDGDSHGP--
gi | 90615 | QHWSAETPHKPQFTFTSAPQAGLEENFCRNPDGDSHGP--

450 460 470 480
NOV5
gi | 15294659 | TRNTQGHSTTVPCDAALMTSRHQ--WTFQTRCSLRSVA
gi | 10337615 | WCYTMDPRTPFDYCALRCADDQPPSILDPPDQVFEKCG
gi | 123114 | WCYTMDPRTPFDYCALRCADDQPPSILDPPDQVFEKCG
gi | 15299258 | TRNTQGHSTTVPCDAALMTSRHQ--WTFQTRCSLRSVA
gi | 90615 | WCYTMDPRTPFDYCALRCADDQPPSILDPPDQVFEKCG

490 500 510 520
.....

Applicants: Guo
U.S.S.N.: 09/981,151

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

RGWIGWISGVPSCAWTCAIRATHPGQSA CGIG-----
KRVDRLDQRRSKLRVVGHPGNSPWTVSLRNRQGOHFCGG
KRVDRLDQRRSKLRVVGHPGNSPWTVSLRNRQGOHFCGG
KRVDRLDQRRSKLRVVGHPGNSPWTVSLRNRQGOHFCGG
RGWIGWISGVPSCAWTCAIRATHPGQSA CGIGQGOHFCGG
K-----RVDNSKLRVVGHPGNSPWTVSLRNRQGOHFCGG

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

..... 530 540 550 560
-----MPLTGYEVWLGTLFONPOHGE
SLVKEQWILTARQCFSSCHMPLTGYEVWLGTLFONPOHGE
SLVKEQWILTARQCFSSCHMPLTGYEVWLGTLFONPOHGE
SLVKEQWILTARQCFSSCHMPLTGYEVWLGTLFONPOHGE
SLVKEQWILTARQCFSSCHMPLTGYEVWLGTLFONPOHGE
SLVKEQWILTARQCFSSCHMPLTGYEVWLGTLFONPOHGE

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

..... 570 580 590 600
PSLQRPVAKMVCGPSGSQVLVLLKLEERSVTINORVALICL
PSLQRPVAKMVCGPSGSQVLVLLKLEERSVTINORVALICL
PSLQRPVAKMVCGPSGSQVLVLLKLEERSVTINORVALICL
PSLQRPVAKMVCGPSGSQVLVLLKLEERSVTINORVALICL
PGLQRPVAKMVCGPSGSQVLVLLKLEERSVTINORVALICL
AQLQRPVAKMVCGPSGSQVLVLLKLEERSVTINORVALICL

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

..... 610 620 630 640
PPEWYVVPPTKCEIAGWGETKGTGNDTVLNVALLNVISN
PPEWYVVPPTKCEIAGWGETKGTGNDTVLNVALLNVISN
PPEWYVVPPTKCEIAGWGETKGTGNDTVLNVALLNVISN
PPEWYVVPPTKCEIAGWGETKGTGNDTVLNVALLNVISN
PPE-----
PPEQYVVPPTKCEIAGWGETKGTGNDTVLNVALLNVISN

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

..... 650 660 670 680
QECNIKHGRG-----RGDYGGPLACFT
QECNIKHGRGRVRESECTEGLVAPVGACEGDYGGPLACFT
QECNIKHGRGRVRESECTEGLVAPVGACEGDYGGPLACFT
QECNIKHGRGRVRESECTEGLVAPVGACEGDYGGPLACFT
QECNIKHGRGRVRESECTEGLVAPVGACEGDYGGPLACFT
QECNIKHGRGRVRESECTEGLVAPVGACEGDYGGPLACFT

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

..... 690 700 710 720
HNCWVLEGIIIPNRVCARSRWPAVFTRVSFVDWIHKVMR
HNCWVLEGIIIPNRVCARSRWPAVFTRVSFVDWIHKVMR
HNCWVLEGIIIPNRVCARSRWPAVFTRVSFVDWIHKVMR
HNCWVLEGIIIPNRVCARSRWPAVFTRVSFVDWIHKVMR
HNCWVLEGIIIPNRVCARSRWPAVFTRVSFVDWIHKVMR
HNCWVLEGIIIPNRVCARSRWPAVFTRVSFVDWIHKVMR

NOV5
gi | 15294659 |
gi | 10337615 |
gi | 123114 |
gi | 15299258 |
gi | 90615 |

LG (SEQ ID NO:16)
LG (SEQ ID NO:51)
LG (SEQ ID NO:52)
LG (SEQ ID NO:53)
-- (SEQ ID NO:54)
LE (SEQ ID NO:55)

Applicants: Guo
U.S.S.N.: 09/981,151

Table 5G. Domain Analysis of NOV5

~~gnl|Pfam|pfam00051~~, kringle, Kringle domain. Kringle domains have been found in plasminogen, hepatocyte growth factors, prothrombin, and apolipoprotein A. Structure is disulfide-rich, nearly all-beta. (SEQ ID NO:85)
CD-Length = 79 residues, 100.0% aligned
Score = 104 bits (259), Expect = 2e-23

Query: 110 CIMNNGVGYRGTMATTVGGLPCQAWSHKFPNDH-KYTPT--LRNGLEENFCRNPDPGDPGG 166
| | | | | + | | | | | + | + | | | | | | | + | | | | |
Sbjct: 1 CYHNGENYRGTA TTESGAPCQRWDSQTPHRHSKYTPERYPAKGLGENYCRNPDGDE-R 59

Query: 167 PWCYTTPDAVRFQSCGIKSC 186 (of SEQ ID NO:16)
| | | | | | | | | + + | | |
Sbjct: 60 PWCYTTPDPRVWEYCDIPRC 79 (SEQ ID NO:79)

At pages 71-72, please replace Table 5H with the following:

Table 5H. Domain Analysis of NOV5

~~gnl|Smart|smart00130~~, KR, Kringle domain; Named after a Danish pastry. Found in several serine proteases and in ROR-like receptors. Can occur in up to 38 copies (in apolipoprotein(a)). Plasminogen-like kringles possess affinity for free lysine and lysine- containing peptides. (SEQ ID NO:86)
CD-Length = 83 residues, 97.6% aligned
Score = 111 bits (278), Expect = 1e-25

Query: 191 CVWCNGEYYRGAVDRTESGRECQRWDLQHPHQHPFEPGKFLDQGLDDNYCRNPDPG-SERP 249
| | | | | | | | | + | + | | | | | | | | | + | + | | + | | | | | | | |
Sbjct: 3 CYAGNGESYRGTA TTKSGKPCQRWDSQTPHLHRFTPERFPGLGLEHNYCRNPDG DSEGP 62

Query: 250 WCYTTDPQIEREFCDLPRCGS 270 (of SEQ ID NO:16)
| | | | | | | + | + | + | + | | |
Sbjct: 63 WCYTTDPNVRWEYCDIPQCES 83 (SEQ ID NO:)

At pages 72, please replace Table 5I with the following:

Applicants: Guo
U.S.S.N.: 09/981,151

Table 5I. Domain Analysis of NOV5

gnl|Smart|smart00130, KR, Kringle domain; Named after a Danish pastry. Found in several serine proteases and in ROR-like receptors. Can occur in up to 38 copies (in apolipoprotein(a)). Plasminogen-like kringles possess affinity for free lysine and lysine- containing peptides.
(SEQ ID NO:86)
CD-Length = 83 residues, 97.6% aligned
Score = 106 bits (265), Expect = 4e-24

Query: 108 RTCIMNNGVGYRGTMAITVGGGLPCQAWSHKFPNDHKYTPTLRN--GLEENFCRNPDGDPG 165
| | | | | + | | | | | + | + | + | | | | + | | | | |
Sbjct: 1 RDCYAGNGESYRGTAATTKSGKPCQRWDSQTPHLHRFTPERFPGLGLEHNYCRNPDGDS 60
Query: 166 GPWCYTTPDAVRFQSCGIKSC 186 (of SEQ ID NO:16)
| | | | | | | | | | + + | | |
Sbjct: 61 GPWCYTTPDNVRWEYCDIPQC 81 (SEQ ID NO:86)

At pages 72, please replace Table 5J with the following:

Table 5J. Domain Analysis of NOV5

gnl|Smart|smart00130, KR, Kringle domain; Named after a Danish pastry. Found in several serine proteases and in ROR-like receptors. Can occur in up to 38 copies (in apolipoprotein(a)). Plasminogen-like kringles possess affinity for free lysine and lysine- containing peptides.
(SEQ ID NO:86)
CD-Length = 83 residues, 97.6% aligned
Score = 104 bits (260), Expect = 1e-23

Query: 283 CFRGKGEGYRGTAATTTAGVPCQRWDAQIPHQHRFTPEKYACKDLRENFCRNPDG-SEAP 341
| + | | | | | + | | + | | | | + | | | | | + + | | + | | | | | |
Sbjct: 3 CYAGNGESYRGTAATTKSGKPCQRWDSQTPHLHRFTPERFPGLGLEHNYCRNPDGDS 62
Query: 342 WCFTLRPGMRAAFQYQIRRCTD 363 (of SEQ ID NO:16)
| | + | | + | + | | + |
Sbjct: 63 WCYTTPDNVRWEYCD-IPQCES 83 (SEQ ID NO:86)

At pages 72-73, please replace Table 5K with the following:

Applicants: Guo
U.S.S.N.: 09/981,151

Table 5K. Domain Analysis of NOV5

~~gnl|Smart|smart00020~~, Tryp_SPc, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues. (SEQ ID NO:87)
CD-Length = 230 residues, 79.1% aligned
Score = 110 bits (274), Expect = 3e-25

```

Query:  504  PLTGYEVWLGTLFQNPQHGEPSLQRPVAKMVCGPSGSQ-----LVLLKLESVTLNQR  557
          +  |  ||+  +  |  |  |++  |  +  +  |||  |||+
Sbjct:  49   APSSIRVRLGSHDLSSGEET---QTVKVKSVIVHPNPNSTYDNDIALKLSEPVTLSDT  105

Query:  558  VALICLPPEWYVVPVPGTKCEIAGWGETKGTG--NDTVLNVALLNVISNQECNIKHRGR--  613
          |  |||  |  ||  |  ++|||  |  +  |  +  ++||  |  +  |
Sbjct:  106  VRPICLPSSGYNVPA GTTCTVSGWGRTSESSGSLPDTLQEVNVP IVSNATCRRAYS GGPA  165

Query:  614  -----GDYGGPLACFTHNCWVLEGIIIPNRV-CARSCWPAVFTRVS  653
          ||  |||  |  ||  ||+  ||  ||  |  |  |++|||
Sbjct:  166  ITDNMLCAGGLEGGKDACQDGGGPLVC-NDPRWVLVGVISWGSYGCARPNKPGVYTRVS  224

Query:  654  VFVDWI  659  (of SEQ ID NO:16)
          ++|||
Sbjct:  225  SYLDWI  230  (SEQ ID NO:87)

```

At pages 73, please replace 5L with the following:

Table 5L. Domain Analysis of NOV5

~~gnl|Pfam|pfam00089~~, trypsin, Trypsin. Proteins recognized include all proteins in families S1, S2A, S2B, S2C, and S5 in the classification of peptidases. Also included are proteins that are clearly members, but that lack peptidase activity, such as haptoglobin and protein Z (PRTZ*). (SEQ ID NO:88)
CD-Length = 217 residues, 77.9% aligned
Score = 92.0 bits (227), Expect = 9e-20

```

Query:  508  YEVWLGTLFQNPQHGEPSLQRPVAKMV---CGPSGSQLVLLKLESVTLNQRVALICL  563
          |  ||  |  |  +  |  +  |  |++  |  +  +  |||+  |||  |  |||
Sbjct:  49   VRVVLGE--HNLGTTEGTEQKFDVKKIIVHPNPNPTNDIALKLKSPVTLGDTVRPICL  106

Query:  564  PPEWYVVPVPGTKCEIAGWGETKGTGNDTVLNVALLNVISNQECNIKHRG-----  612
          |  +  |  ||  |  ++|||  ||  |  |  ++  ++|  +  |  +  |
Sbjct:  107  PSASSDLPVGTTC SVSGWGRTKNLGTS DTLQEVVVP IVSRETCRSAYGGTVTDTMICAGA  166

Query:  613  -----RGDYGGPLACFTHNCWVLEGIIIPNRVCARSCWPAVFTRVS VFVDWI  659
          +||  |||  |  |  ||+  ||  +  |  |  |++||  ++|||
Sbjct:  167  LGGKDACQDGGGPLVCSDG---ELVGVISWGYGCAVGNYPGVYTRVSRYLDWI  217

Query:  (of SEQ ID NO:16)
Sbjct:  (SEQ ID NO:88)

```

Applicants: Guo
U.S.S.N.: 09/981,151

At pages 73, please replace Table 5M with the following:

Table 5M. Domain Analysis of NOV5

~~gnl|Smart|smart00473~~, PAN_AP, divergent subfamily of APPLE domains; Apple-like domains present in Plasminogen, C. elegans hypothetical ORFs and the extracellular portion of plant receptor-like protein kinases. Predicted to possess protein- and/or carbohydrate-binding functions. (SEQ ID NO:89)
CD-Length = 79 residues, 94.9% aligned
Score = 52.0 bits (123), Expect = 1e-07

Query: 25 DFQVLRGTELQHLLHAVVPGPWQEDVADAEECAGRC-GPLMDCRAFHYNVSSHGCQLLPW 83
| | |+| | | | | |+| | | + | | |
Sbjct: 5 CFVRLPNTKL-----PDFSPIVISVASLEECAQKCLNSNCSCRSFTYNNDTKGCLLWSE 58

Query: 84 TQHSPTHRLRRSGRCDLFQKK 104 (of SEQ ID NO:16)
+ +| || | ++|
Sbjct: 59 SSLGDARQLLPSSGGVDYYEKI 79 (SEQ ID NO:89)

At pages 74, please replace Table 5N with the following:

Table 5N. Domain Analysis of NOV5

~~gnl|Pfam|pfam00024~~, PAN, PAN domain. The PAN domain contains a conserved core of three disulphide bridges. In some members of the family there is an additional fourth disulphide bridge the links the N and C termini of the domain. The domain is found in diverse proteins, in some they mediate protein-protein interactions, in others they mediate protein-carbohydrate interactions. (SEQ ID NO:159)
CD-Length = 78 residues, 76.9% aligned
Score = 50.1 bits (118), Expect = 4e-07

Query: 45 PWQEDVADAEECAGRCGPLMD-CRAFHYNVSSHGCQLLPWTQHSPTHRLRRSGRCDLFQK 103
+| |||| | ||+| || | | + | | | + | ++|
Sbjct: 17 ISVVNVPSLEECAALCLEEPRVCRSFTYNNKSKQCLLKSESSGSLPRLKRPSQKVDYYEK

Query: (of SEQ ID NO:16)
Sbjct: (SEQ ID NO:159)

At page 78 please replace Table 6C with the following:

Table 6C. BLAST results for NOV6					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 13651468 ref XP_016351.1 XP 016351	similar to GASTRIN/CHOLECYST OKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK- BR) (H. sapiens) [Homo sapiens]	135	122/135 (90%)	126/135 (92%)	1e-58
gi 4557581 ref NP_01435.1 NP 001435	fatty acid binding protein 5 (psoriasis- associated); E- FABP [Homo sapiens]	135	124/135 (91%)	126/135 (92%)	1e-58
gi 13651882 ref XP_011655.5 XP 011655	fatty acid binding protein 5 (psoriasis- associated) [Homo sapiens]	135	119/135 (88%)	124/135 (91%)	6e-57
gi 13651563 ref XP_015760.1 XP 015760	similar to GASTRIN/CHOLECYST OKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK- BR) (H. sapiens) [Homo sapiens]	135	118/135 (87%)	125/135 (92%)	5e-56
gi 6648071 sp P55052 FABP-BOVIN P55052	FATTY ACID- BINDING PROTEIN, EPIDERMAL (E- FABP)	135	117/135 (86%)	124/135 (91%)	1e-55

At page 79 please replace Table 6D with the following:

Table 6D Information for the ClustalW proteins

- NOV6 (SEQ ID NO:18)
- ~~gi|13651468|ref|XP_016351.1|~~ gi|13651468| XP 016351 similar to
GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR) (H. sapiens) [Homo sapiens] (SEQ ID NO:56)
- ~~gi|4557581|ref|NP_001435.1|~~ gi|4557581| NP 001435 fatty acid binding protein 5
(psoriasis-associated); E-FABP [Homo sapiens] (SEQ ID NO:57)
- ~~gi|13651882|ref|XP_011655.5|~~ gi|13651882| XP 011655 fatty acid binding protein 5
(psoriasis-associated) [Homo sapiens] (SEQ ID NO:58)
- ~~gi|13651563|ref|XP_015760.1|~~ gi|13651563| XP 015760 similar to
GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-BR) (H. sapiens) [Homo sapiens] (SEQ ID NO:59)
- ~~gi|6648071|sp|P55052|~~ FABP-BOVIN gi|13651563| P55052 FATTY ACID-BINDING PROTEIN,
EPIDERMAL (E-FABP) (SEQ ID NO:60)

	10	20	30	40
NOV6
gi 13651468	MATVQQL	CGRWRLVDSK	RFDEYMKEL	GVGIALRKMGAMAK
gi 4557581	MATVQQL	CGRWRLVDSK	GFDEYMKEL	GVGIALRKMGAMAK
gi 13651882	MATVQQL	CGRWRLVDSK	GFDEYMKEL	GVGIALRKMGAMAK
gi 13651563	MATVQQL	CGRWRLVDSK	GFDEYMKEL	GVGIALRKMGAMAK

Applicants: Guo
U.S.S.N.: 09/981,151

```
gi|6648071| MATVQQLVGRWRLVSKGFDEYMKGVGVALRKVGAMAK
                    50      60      70      80
NOV6      PDCIITCDGKNLTIKTESTLKTQFSC TLGEKFEETTADG
gi|13651468| PDCIITCDGKNLTIKTESTLKTQFSC TLGEKFEETTADG
gi|4557581| PDCIITCDGKNLTIKTESTLKTQFSC TLGEKFEETTADG
gi|13651882| PDCIITCDGKNLTIKTESTLKTQFSC TLGEKFEETTADG
gi|13651563| PDCIITCDGKNLTIKTESTLKTQFSC TLGEKFEETTADG
gi|6648071| PDCIITSDGKNLSIKTESTLKTQFSC TLGEKFEETTADG
                    90     100     110     120
NOV6      RKTQTVCSFADGALVQHQEWGDKENTITRKLKDGKLVVVC
gi|13651468| RKTQTVCNFTDGALVQHQEWGDKESTITRKLKDGKLVVVC
gi|4557581| RKTQTVCNFTDGALVQHQEWGDKESTITRKLKDGKLVVVC
gi|13651882| RKTQTVCNFTDGALVQHQEWGDKENTITRKLKDGKLVVVC
gi|13651563| RKTQTVCNFTDGALVQHQEWGDKESTITRKLKDGKLVVVC
gi|6648071| RKTQTVCNFTDGALVQHQEWGDKESTITRKLKDGKLVVVC
                    130
NOV6      VMNNVACTRIYEKVE (SEQ ID NO:18)
gi|13651468| VMNNVACTRIYEKVE (SEQ ID NO:56)
gi|4557581| VMNNVTCTRIYEKVE (SEQ ID NO:57)
gi|13651882| VMNNVTCTRIYEKVE (SEQ ID NO:58)
gi|13651563| VMNNVTCTRIYEKVE (SEQ ID NO:59)
gi|6648071| VMNNVTCTRIYEKVE (SEQ ID NO:60)
```

Page 80, please replace Table 6E with the following:

Table 6E. Domain Analysis of NOV6

gnl|Pfam|pfam00061, lipocalin, Lipocalin / cytosolic fatty-acid binding protein family. Lipocalins are transporters for small hydrophobic molecules, such as lipids, steroid hormones, bilins, and retinoids. Alignment subsumes both the lipocalin and fatty acid binding protein signatures from PROSITE. This is supported on structural and functional grounds. Structure is an eight-stranded beta barrel. (SEQ ID NO:90)
CD-Length = 145 residues, 76.6% aligned
Score = 53.1 bits (126), Expect = 1e-08

```
Query: 9 GRWRLVDSKRFDEYMK-EGGVGTALRKMDAMAK-PDCIITCDGKNLTIKTESTLKTQFSC 66
      | + | | | | | + | | | | | | + | | | | + | + +
Sbjct: 4 GKWYLVASANFDPKLKEELGVLEATRKEITPLKEGNLEIVFDGDKNGICEETFGKLEKTK 63

Query: 67 TLGEKFEETTADGRKTQTVCSFADGALVQHQEWGDKENTITRKLKDGKLVV 117
      | | + + | | | + + | | + | | + | + | +
Sbjct: 64 KLGVEFDYYTGDNRFFVVLDTDYDNYLLVCVQKGDGNETSRTAELYGRTPEL 114
```

Query: (of SEQ ID NO:18)

Sbjct: (SEQ ID NO:90)

At page 84 please replace Table 7C with the following:

Table 7C. BLAST results for NOV7					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 12229761 sp Q9NTQ9 CXB4_HUMAN Q9NTQ9	GAP JUNCTION BETA-4 PROTEIN (CONNEXIN 30.3) (CX30.3)	266	266/266 (100%)	266/266 (100%)	e-155
gi 544118 sp P36380 CXB5_RAT P36380	GAP JUNCTION BETA-5 PROTEIN (CONNEXIN 30.3) (CX30.3)	265	230/266 (86%)	245/266 (91%)	e-132
gi 6680015 ref NP_032153.1 NP 032153	gap junction membrane channel protein beta 4; connexin 30.3 [Mus musculus]	266	230/266 (86%)	244/266 (91%)	e-131
gi 10835079 ref NP_05259.1 NP 05259	gap junction protein, beta 5 (connexin 31.1) [Homo sapiens]	273	153/226 (67%)	177/226 (77%)	3e-88
gi 4009522 gb AAC95472.1 (AF099731) AAC95472	connexin 31.1 [Homo sapiens]	273	152/226 (67%)	176/226 (77%)	1e-87

At page 85 please replace Table 7D with the following:

Table 7D. Information for the ClustalW proteins

- NOV7 (SEQ ID NO:20)
- ~~gi|12229761|sp|Q9NTQ9|CXB4_HUMAN Q9NTQ9~~ GAP JUNCTION BETA-4 PROTEIN (CONNEXIN 30.3) (CX30.3) (SEQ ID NO:61)
- ~~gi|544118|sp|P36380|CXB5_RAT Q9NTQ9~~ GAP JUNCTION BETA-5 PROTEIN (CONNEXIN 30.3) (CX30.3) (SEQ ID NO:62)
- ~~gi|6680015|ref|NP_032153.1| NP 032153~~ gap junction membrane channel protein beta 4; connexin 30.3 [Mus musculus] (SEQ ID NO:63)
- ~~gi|10835079|ref|NP_05259.1| NP 05259~~ gap junction protein, beta 5 (connexin 31.1) [Homo sapiens] (SEQ ID NO:64)
- ~~gi|4009522|gb|AAC95472.1| AAC95472~~ (AF099731) connexin 31.1 [Homo sapiens] (SEQ ID NO:65)

	10	20	30	40
NOV7
gi 12229761	MNWAFLQGLLSGVNKYSTVLSRIWLSVVFIFRVLVYVAA			
gi 544118	MNWAFLQGLLSGVNKYSTVLSRIWLSVVFIFRVLVYVAA			
gi 6680015	MNWAFLQGLLSGVNKYSTALGRIWLSVVFIFRVLVYVAA			
gi 10835079	MNWSIFEGLLSGVNKYSTALGRIWLSVVFIFRVLVYVAA			
gi 4009522	MNWSIFEGLLSGVNKYSTALGRIWLSVVFIFRVLVYVAA			
	50	60	70	80
NOV7	EEVWDDIEQKDFMCNTKQPGCPNVCYDEFFPVSHVRLWALQ			
gi 12229761	EEVWDDIEQKDFMCNTKQPGCPNVCYDEFFPVSHVRLWALQ			

Applicants: Guo
U.S.S.N.: 09/981,151

```
gi|544118|EEVWDDDEQKDFICNTKQPGCPNVCYDEFFPVSHVRLWALO
gi|6680015|EEVWDDDEQKDFICNTKQPGCPNVCYDEFFPVSHVRLWALO
gi|10835079|ERVWSDDEKDFICNTRQPGCSNVCEDEFFPVSHVRLWALO
gi|4009522|XRVWSDDEKDFICNTRQPGCSNVCEDEFFPVSHVRLWALO
```

```

          90      100      110      120
NOV7      LILVTCPSLLVVMHVAYREERERKHELKHGPNAPSLYDNL
gi|12229761|LILVTCPSLLVVMHVAYREERERKHELKHGPNAPSLYDNL
gi|544118|LILVTCPSLLVVMHVAYREERERKHLRKHGPDAPALYSNL
gi|6680015|LILVTCPSLLVVMHVAYREERERKHLRKHGPNAPALYSNL
gi|10835079|LILVTCPSLLVVMHVAYREVEKGRHREAHGENSGRLYLNP
gi|4009522|LILVTCPSLLVVMHVAYREVEKGRHREAHGENSGRLYLNP

```

```

          130      140      150      160
NOV7      SKKRGGGLWWTYLLSLIFKAAVDGFLYIFHRYKYDYDMPR
gi|12229761|SKKRGGGLWWTYLLSLIFKAAVDGFLYIFHRYKYDYDMPR
gi|544118|SKKRGGGLWWTYLLSLIFKAAVDGFLYIFHRYKYDYDMPR
gi|6680015|SKKRGGGLWWTYLLSLIFKAAVDGFLYIFHRYKYDYDMPR
gi|10835079|GKKRGGGLWWTYVCSLVFKASVDIAFLYVHESFYPKYITPP
gi|4009522|GKKRGGGLWWTYVCSLVFKASVDIAFLYVHESFYPKYITPP

```

```

          170      180      190      200
NOV7      VVACSVPCPHTVDCYISRPTEKKVFTYFMVTTAAICILL
gi|12229761|VVACSVPCPHTVDCYISRPTEKKVFTYFMVTTAAICILL
gi|544118|VVACSVPCPHTVDCYISRPTEKKVFTYFMVTTAAICILL
gi|6680015|VVACSVPCPHTVDCYISRPTEKKVFTYFMVTTAAICILL
gi|10835079|VVKCHADPCPNIVDCIISKPSSEKNIEFTLFMVATAAICILL
gi|4009522|VVKCHADPCPNIVDCIISKPSSEKNIEFTLFMVATAAICILL

```

```

          210      220      230      240
NOV7      NLSEVFYLVGKRCMEIFGPRHRRPRCRECLPD---TCPP
gi|12229761|NLSEVFYLVGKRCMEIFGPRHRRPRCRECLPD---TCPP
gi|544118|NLSEVAYLVGKRCMEVFRPRROKTSRRHOLED---TCPP
gi|6680015|NLSEVVYLVGKRCMEVFRPRRKAASRRHOLED---TCPP
gi|10835079|NLVEIIYLVSKRCHECLAARKAAMCTGHHPHGTTSSCKQ
gi|4009522|NLVEIIYLVSKRCHECLAARKAAMCTGHHPHGTTSSCKQ

```

```

          250      260      270
NOV7      YVLSGGG---HPEDGNSVLMKAGSAPVDAGGYF (SEQ ID NO:20)
gi|12229761|YVLSGGG---HPEDGNSVLMKAGSAPVDAGGYF (SEQ ID NO:61)
gi|544118|YVLSKGG---HPODESTVLTAKAGMATVDAGVYP (SEQ ID NO:62)
gi|6680015|YVLSKGG---HPODESVLTAKAGMATVDAGVYP (SEQ ID NO:63)
gi|10835079|DDLLSGDLIFLGSDSHPPFLPDRPRDEVKKTIL- (SEQ ID NO:64)
gi|4009522|DDLLSGDLIFLGSDSHPPFLPDRPRDEVKKTIL- (SEQ ID NO:65)

```

At page 86 please replace Table 7E with the following:

Applicants: Guo
U.S.S.N.: 09/981,151

Table 7E. Domain Analysis of NOV7

~~gnl|Pfam|pfam00029~~, connexin, Connexin. (SEQ ID NO:91)
CD-Length = 218 residues, 100.0% aligned
Score = 318 bits (814), Expect = 3e-88

```

Query:  1  MNWAFLOGLLSGVNKYSTVLSRIWLSVVFIFRVLVYVVAEEVWDDEQKDFVCNTKQPGC  60
      |||+||| || |||+|| + +|||+|||+|| ||| || ||| |||+|||
Sbjct:  1  MDWSFLGRLLLEGVNHSTAIGKIWLSVLFIIRILVLGVAESVWGDEQSDFCNTQQPGC  60

Query: 61  PNVCYDEFFPVSHVRLWALQLILVTCPSLLVVMHVAYREERERKHHLKHGPNAPSLYDNL 120
      |||+|||+||| ||| ||| + ||| + ||| ||| ||| ++ ||
Sbjct: 61  ENVCYDQFFPISHVRLWVLQLIFVSTPSLLYLGHVAYRVRREEKLREKEEHKGLYSEE 120

Query: 121 SKK-----RGGLWWTYLLSLIFKAAVDAGFLYIFHRLYKDYDMPRVVACSVEPC 169
      +|| ||| |||+ |||+ + ||| + || + || + || ||
Sbjct: 121 AKKRCGSEDGKVRIRGGLWWTYVFSIIFKSI FEVGFLYGQYLLY-GFTMSPLVVC SRAPC 179

Query: 170 PHTVDCYISRPTTEKKVFTYFMVTTAAICILLNLSEVFYL 208 (of SEQ ID NO:20)
      |||+|||+||| + || + |||+|||+|||+|||
Sbjct: 180 PHTVDCFVSRPTEKTIFIVFMLVVSAICLLNLNLAELFYL 218 (SEQ ID NO:91)

```

At page 87, please replace Table 7F with the following:

Table 7F. Domain Analysis of NOV7

~~gnl|Smart|smart00037~~, CNX, Connexin homologues; Connexin channels participate in the regulation of signaling between developing and differentiated cell types. (SEQ ID NO:160)
CD-Length = 34 residues, 100.0% aligned
Score = 79.0 bits (193), Expect = 3e-16

```

Query:  42  EVWDDEQKDFVCNTKQPGCPNVCYDEFFPVSHVR  75  (of SEQ ID NO:20)
      || ||| || |||+||| |||+|||+|||
Sbjct:  1  SVWGDEQSDFTCNTQQPGCENVCYDQFFPISHVR  34  (SEQ ID NO:160)

```

At page 100, please replace Table 9C with the following:

Table 9C. BLAST results for NOV9

Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
gi 13591536 emb CAC36351.1 CAC36351 (AL109613)	dJ1033H22.1 (KIAA0554 protein) [Homo sapiens]	434	373/430 (86%)	375/430 (86%)	0.0

Applicants: Guo
U.S.S.N.: 09/981,151

gi 8923249 ref NP_060207.1 NP 060207	hypothetical protein FLJ20275 [Homo sapiens]	330	328/330 (99%)	329/330 (99%)	e-175
gi 10435680 dbj BAB14638.1 BAB14638 (AK023681)	unnamed protein product [Homo sapiens]	592	319/595 (53%)	432/595 (71%)	e-160
gi 13936547 gb AAK49824.1 AF265550.1 AAK49824 (AF265550)	formin-binding protein 17 [Homo sapiens]	679	307/624 (49%)	422/624 (67%)	e-148
gi 3043632 dbj BAA25480.1 BAA25480 (AB011126)	KIAA0554 protein [Homo sapiens]	674	307/624 (49%)	422/624 (67%)	e-148

At page 100 please replace Table 9D with the following:

Table 9D. ClustalW Analysis of NOV9

- 1) Novel NOV9 (SEQ ID NO:24)
- 3) ~~gi|13591536|emb|CAC36351.1|~~ CAC36351 ~~gi|13591536|~~ (AL109613) dJ1033H22.1 (KIAA0554 protein) [Homo sapiens] (SEQ ID NO:66)
- 4) ~~gi|8923249|ref|NP_060207.1|~~ NP 060207 ~~gi|8923249|~~ hypothetical protein FLJ20275 [Homo sapiens] (SEQ ID NO:67)
- 5) ~~gi|10435680|dbj|BAB14638.1|~~ BAB14638 ~~gi|10435680|~~ (AK023681) unnamed protein product [Homo sapiens] (SEQ ID NO:68)
- 6) ~~gi|13936547|gb|AAK49824.1|AF265550.1|~~ AAK49824 ~~gi|13936547|~~ (AF265550) formin-binding protein 17 [Homo sapiens] (SEQ ID NO:69)
- 7) ~~gi|3043632|dbj|BAA25480.1|~~ BAA25480 ~~gi|3043632|~~ (AB011126) KIAA0554 protein [Homo sapiens] (SEQ ID NO:70)

	10	20	30	40
NOV9			
gi 13591536	-----			
gi 8923249	-----			
gi 10435680	-----			
gi 13936547	LWNGGEEEEPPRRPRARSCEPEEAARTPGFPPSRGSRGAKG			
gi 3043632	-----EEEP RRPRARSCEPEEAARTPGFPPSRGSRGAKG			
	50	60	70	80
NOV9			
gi 13591536	-----MSWGT	ELWDQFD	SLDKHT	
gi 8923249	-----			
gi 10435680	-----MSWGT	ELWDQFD	NLEKHT	
gi 13936547	SPGRG	TREPRPPRGAPLRVPCTMSWGT	ELWDQFD	NLEKHT
gi 3043632	SPGRG	TREPRPPRGAPLRVPCTMSWGT	ELWDQFD	NLEKHT
	90	100	110	120
NOV9			
gi 13591536	QWGID	FLERYAKFVKERT	ETIEQ	NYAKQLRNLVKKYCPKRS
gi 8923249	-----			
gi 10435680	QWGID	ILEKYIKFVKERT	ETIEL	SYAKQLRNLVKKYCPKRN
gi 13936547	QWGID	ILEKYIKFVKERT	ETIEL	SYAKQLRNLVKKYCPKRN
gi 3043632	QWGID	ILEKYIKFVKERT	ETIEL	SYAKQLRNLVKKYCPKRN

Applicants: Guo
U.S.S.N.: 09/981,151

```

      130      140      150      160
NOV9      .....|.....|.....|.....|
gi 13591536|SKDEE-PRFTSCVAFNTILNELNDYAGOREVVAEEMAHRY|
gi 8923249|-----|
gi 10435680|SKKEEYKTSCKAFISNLNELNDYAGOREVISENMAST|
gi 13936547|SKKEEYKTSCKAFISNLNELNDYAGOREVISENMAST|
gi 3043632|SKKEEYKTSCKAFISNLNELNDYAGOREVISENMAST|

      170      180      190      200
NOV9      YGELMRVAEDLKTERKMLQEGRKAQQEEDMCWKQMGNSK
gi 13591536|-----|
gi 8923249|-----|
gi 10435680|IVDLARYVQELKQERKSNFHDGRKAQQEETTCWKQHESSK|
gi 13936547|IVDLARYVQELKQERKSNFHDGRKAQQEETTCWKQHESSK|
gi 3043632|IVDLARYVQELKQERKSNFHDGRKAQQEETTCWKQHESSK|

      210      220      230      240
NOV9      XKFERSCREAEKAAQSYERIDNDTNATKADVENAKQQLNL
gi 13591536|-----|
gi 8923249|-----|
gi 10435680|RRFERDCKEADRAQQYEKQDADINVTKADVEKARQQAQI|
gi 13936547|RRFERDCKEADRAQQYEKQDADINVTKADVEKARQQAQI|
gi 3043632|RRFERDCKEADRAQQYEKQDADINVTKADVEKARQQAQI|

      250      260      270      280
NOV9      RTHMADENKNAYAAQLQNFNGEQQHKTAVVVIPIQIKQIQE
gi 13591536|-----|
gi 8923249|-----|
gi 10435680|RHOMAKDSKADYSSILOKFNHEQHEVMTHTIPNIEQKIQE|
gi 13936547|RHOMAKDSKADYSSILOKFNHEQHEVMTHTIPNIEQKIQE|
gi 3043632|RHOMAKDSKADYSSILOKFNHEQHEVMTHTIPNIEQKIQE|

      290      300      310      320
NOV9      MDERRITGLSECYRGFADSERKVIPIISKCLGEMHAAKS
gi 13591536|-----|
gi 8923249|-----|
gi 10435680|MEERRIVRMGESMKTVAEVDROVIPITICKCLDGIVKAAES|
gi 13936547|MEERRIVRMGESMKTVAEVDROVIPITICKCLDGIVKAAES|
gi 3043632|MEERRIVRMGESMKTVAEVDROVIPITICKCLDGIVKAAES|

      330      340      350      360
NOV9      VDERRDSQVVDSEKSGFEPPGDFPFEDYSOHTYRTISDG
gi 13591536|-----|
gi 8923249|-----|
gi 10435680|VDERRDSQVVDSEKSGFEPPGDFPFEDYSOHTYRTISDG|
gi 13936547|VDERRDSQVVDSEKSGFEPPGDFPFEDYSOHTYRTISDG|
gi 3043632|VDERRDSQVVDSEKSGFEPPGDFPFEDYSOHTYRTISDG|

      370      380      390      400
NOV9      TISASKQESGKMDAKTPVGKAKGKLWLFCKKPK
gi 13591536|-----|
gi 8923249|-----|
gi 10435680|TISASKQESGKMDAKTTVGKAKGKLWLFCKKPK|
gi 13936547|TISASKQESGKMDAKTTVGKAKGKLWLFCKKPK|
gi 3043632|TISASKQESGKMDAKTTVGKAKGKLWLFCKKPK|

      410      420      430      440
NOV9      SPNSNRCE-GKPDLKFG-GKSKGKLWPFIKKNKLMSSLLTS
gi 13591536|-----|
gi 8923249|-----|
gi 10435680|SPNSNRCE-GKPDLKFG-GKSKGKLWPFIKKNKLMSSLLTS|
gi 13936547|SPNSNRCE-GKPDLKFG-GKSKGKLWPFIKKNKLMSSLLTS|
gi 3043632|SPNSNRCE-GKPDLKFG-GKSKGKLWPFIKKNKLMSSLLTS|
```

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NOV9

```
gi | 13591536 | --QSPPLTPTSLFTSSTPNGSQFLTFSTEPHYCMNEIKT  
gi | 8923249 | -----  
gi | 10435680 | -----KSPKQOKEPTSSRFNEFMT  
gi | 13936547 | PHQPPPPPPASASPSAVPNGPQSPKQOKEPTSSRFNEFMT  
gi | 3043632 | PHQPPPPPPASASPSAVPNGPQSPKQOKEPTSSRFNEFMT
```

NOV9

```
gi | 13591536 | -----G-----PALEDFSSLPPEQRRKKLQQ  
gi | 8923249 | GKPRIPSFRSLKRGG-----PALEDFSSLPPEQRRKKLQQ  
gi | 10435680 | -----G-----PALEDFSSLPPEQRRKKLQQ  
gi | 13936547 | SKPKIHCFRSLKRGLSLKLGATPEDFSSLPPEQRRKKLQQ  
gi | 3043632 | SKPKIHCFRSLKRGLSLKLGATPEDFSSLPPEQRRKKLQQ
```

NOV9

```
gi | 13591536 | MDELNREETOKESDQDAENNKMKDVYEKKNPOMGDPGSLQP  
gi | 8923249 | MDELNREETOKESDQDAENNKMKDVYEKKNPOMGDPGSLQP  
gi | 10435680 | MDELNREETOKESDQDAENNKMKDVYEKKNPOMGDPGSLQP  
gi | 13936547 | MDELNREETOKEMDQDAENNKMKDVYEKKNPOMGDPASLDH  
gi | 3043632 | MDELNREETOKEMDQDAENNKMKDVYEKKNPOMGDPASLDH
```

NOV9

```
gi | 13591536 | KLAETMNNIDRLRMEIHKNEAWLSEVECKTGGRCD--RRH  
gi | 8923249 | KLAETMNNIDRLRMEIHKNEAWLSEVECKTGGRCD--RRH  
gi | 10435680 | KLAETMNNIDRLRMEIHKNEAWLSEVECKTGGRCD--RRH  
gi | 13936547 | KLAEVSONIEKLRVETOKFEAWLAEVECKLPARSEQARRQ  
gi | 3043632 | KLAEVSONIEKLRVETOKFEAWLAEVECKLPARSEQARRQ
```

NOV9

```
gi | 13591536 | SSDIN-----HLVTOGRESPEGSYTDANOEVRGPPQQ  
gi | 8923249 | SSDIN-----HLVTOGRESPEGSYTDANOEVRGPPQQ  
gi | 10435680 | SGLYDSQNPPTVNNCAQDRESPDGSYTEEQSOES-----EM  
gi | 13936547 | SGLYDSQNPPTVNNCAQDRESPDGSYTEEQSOES-----EM  
gi | 3043632 | SGLYDSQNPPTVNNCAQDRESPDGSYTEEQSOES-----EM
```

NOV9

```
gi | 13591536 | HGHHNEFDDEFDDDEPLPAIGHCKAIVPEFGHNEGTAMK  
gi | 8923249 | HGHHNEFDDEFDDDEPLPAIGHCKAIVPEFGHNEGTAMK  
gi | 10435680 | HGHHNEFDDEFDDDEPLPAIGHCKAIVPEFGHNEGTAMK  
gi | 13936547 | KVLATDFDDEFDDDEPLPAIGTCKAIVTEFGONEGTISVV  
gi | 3043632 | KVLATDFDDEFDDDEPLPAIGTCKAIVTEFGONEGTISVV
```

NOV9

```
gi | 13591536 | EGEVLYIIEEDKGDGWTRARRONEEGYVPTSYMEVCLDK  
gi | 8923249 | EGEVLYIIEEDKGDGWTRARRONEEGYVPTSYMEVCLDK  
gi | 10435680 | EGEVLYIIEEDKGDGWTRARRONEEGYVPTSYMEVCLDK  
gi | 13936547 | EGETLYIIEEDKGDGWTRARRONEEGYVPTSYMEVCLDK  
gi | 3043632 | EGETLYIIEEDKGDGWTRARRONEEGYVPTSYMEVCLDK
```

.....

Applicants: Guo
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NOV9	NSKGS-----	(SEQ ID NO:24)
gi 13591536	NSKGVVTYI	(SEQ ID NO:66)
gi 8923249	NSKGS-----	(SEQ ID NO:67)
gi 10435680	NSKGVVTYI	(SEQ ID NO:68)
gi 13936547	NAKDS-----	(SEQ ID NO:69)
gi 3043632	NAKDS-----	(SEQ ID NO:70)

At page 103, please replace Table 9E with the following:

Table 9E. Domain Analysis of NOV9

gnl|Smart|smart00326, SH3, Src homology 3 domains; Src homology 3 (SH3) domains bind to target proteins through sequences containing proline and hydrophobic amino acids. Pro-containing polypeptides may bind to SH3 domains in 2 different binding orientations. (SEQ ID NO:92)
CD-Length = 59 residues, 88.1% aligned
Score = 64.7 bits (156), Expect = 1e-11

Query: 484 HCKAIYPFDGHNEGTLMKEGEVLYIIIEEDKGDGWTRARRQNGEEGYVPTS YI 536
 +|+| + + | + |+++ ++|+ ||| + | |+| |++|+
Sbjct: 4 QVRALYDYTAQDPDELSFKKGDIIITVLEKS-DDGWWKGRGLGTGKEGLFPSNYV 55

Query: (of SEQ ID NO:24)

Sbjct: (SEQ ID NO:92)

At page 104, please replace Table 9F with the following:

Table 9F. Domain Analysis of NOV9

gnl|Pfam|pfam00018, SH3, SH3 domain. SH3 (Src homology 3) domains are often indicative of a protein involved in signal transduction related to cytoskeletal organization. First described in the Src cytoplasmic tyrosine kinase. The structure is a partly opened beta barrel. (SEQ ID NO:93)
CD-Length = 57 residues, 91.2% aligned
Score = 63.5 bits (153), Expect = 3e-11

Query: 486 KAIYPFDGHNEGTLMKEGEVLYIIIEEDKGDGWTRARRQNGEEGYVPTS YID 537
 A+Y + L+ K+G+++ ++E+ GW + R + +EG +P++Y++
Sbjct: 4 VALYDYQARESDELSFKKGDIIIVLEKSDDGWWKGRGLGTGKEGLIPSNYVE 55

Query: of SEQ ID NO:24)

Sbjct: (SEQ ID NO:93)

At page 104, please replace Table 9 with the following:

Table 9G. Domain Analysis of NOV9	
gnl Smart smart00055 , FCH, Fes/CIP4 homology domain; Alignment extended from original report. Highly alpha-helical. Also known as the RAEYL motif or the S. pombe Cdc15 N-terminal domain. (SEQ ID NO:94) CD-Length = 91 residues, 97.8% aligned Score = 58.2 bits (139), Expect = 1e-09	

Query: 1 MSWGTELWDQFDSLDKHTQWGIDFLERYAKFVKERIEIEQNYAKQLRNLVKKYCPKRSSK 60
 | + + || | | ++ | + | | | ++ | | + | | + | | +
 Sbjct: 1 MGFWSELDDGFEALLSRLKNGLRLLLEDLKKFMRERAKIEEYAKKLQKLSKK--LRAVRD 58

Query: 61 DEEPRFTSCVAFFNILNELNDYAGQREVVAE 91 (of SEQ ID NO:24)
 | + | + + | + | | ++ |
 Sbjct: 59 TESELGSLRKAWEVLLSETDALAKQHLQLSE 89 (SEQ ID NO:94)

At page 104, please replace Table 9H with the following:

Table 9H. Domain Analysis of NOV9	
gnl Pfam pfam00611 , FCH, Fes/CIP4 homology domain. Alignment extended from. Highly alpha-helical. (SEQ ID NO:95) CD-Length = 94 residues, 97.9% aligned Score = 40.0 bits (92), Expect = 3e-04	

Query: 1 MSWGTELWDQ-FDSLDKHTQWGIDFLERYAKFVKERIEIEQNYAKQLRNLVKKYCPKRSS 59
 | + | + | | + + | + | | | + | | + | | + | ++ | + ++
 Sbjct: 1 MGFGSELCPGCHKALLSRQDNELRLLEEMKKFMAERAKIEKEYAGKLQHLQAQVGKGPAT 60

Query: 60 KDEEPRFTSCVAFFNILNELNDYAGQREVVAE 91 (of SEQ ID NO:24)
 + | + | ++ | | + + ++ |
 Sbjct: 61 AEGEDELSSLKSWAVILSETEQQSKIHLQISE 92 (SEQ ID NO:95)

At page 113 please replace Table 10F with the following:

Table 10F. BLAST results for NOV10a					
Gene Index/ Identifier	Protein/ Organism	Length (aa)	Identity (%)	Positives (%)	Expect
<u>gi 13540535 ref NP-110397.1 </u> NP 110397	transmembrane protease, serine 5; spinesin [Homo sapiens]	457	452/463 (97%)	453/463 (97%)	0.0
<u>gi 13878822 sp Q9ER04 TMS5-MOUSE</u> Q9ER04	TRANSMEMBRANE PROTEASE, SERINE 5 (SPINESIN)	455	360/461 (78%)	394/461 (85%)	0.0
<u>gi 13507652 ref NP-109634.1 </u> NP 109634	transmembrane protease, serine 5 (spinesin) [Mus musculus]	445	354/451 (78%)	388/451 (85%),	0.0
<u>gi 14770563 ref XP-041427.1 </u> XP 041427	transmembrane protease, serine 5 [Homo sapiens]	398	354/362 (97%)	355/362 (97%)	0.0
<u>gi 12248777 dbj BAB20276.1 </u> BAB20276 (AB016229)	type 2 spinesin [Mus musculus]	311	260/317 (82%)	281/317 (88%)	e-146

At page 114 please replace Table 10G with the following:

Table 10G. ClustalW Analysis of NOV10

- 1) Novel NOV10a (SEQ ID NO:27)
- 2) Novel NOV10b (SEQ ID NO:29)
- 4) gi|13540535|ref|NP-110397.1| NP 110397 gi|13540535| transmembrane protease, serine 5; spinesin [Homo sapiens] (SEQ ID NO:71)
- 5) gi|13878822|sp|Q9ER04|TMS5-MOUSE Q9ER04 gi|13878822| TRANSMEMBRANE PROTEASE, SERINE 5 (SPINESIN) (SEQ ID NO:72)
- 6) gi|13507652|ref|NP-109634.1| NP 109634 gi|13507652| transmembrane protease, serine 5 (spinesin) [Mus musculus] (SEQ ID NO:73)
- 7) gi|14770563|ref|XP-041427.1| XP 041427 gi|14770563| transmembrane protease, serine 5 [Homo sapiens] (SEQ ID NO:74)
- 8) gi|12248777|dbj|BAB20276.1| BAB20276 gi|12248777| (AB016229) type 2 spinesin [Mus musculus] (SEQ ID NO:75)

	10	20	30	40
NOV10a
NOV10b	MSLMDDQPPMEAOYAEEGPGPGIFRAEPGDQOHPIISOAV			
gi 13540535	MSLMDDQPPMEAOYAEEGPGPGIFRAEPGDQOHPIISOAV			
gi 13878822	MSPTLDDQSPMEIRCTEEGAGPGIFRMELGDQOSISQSQ			
gi 13507652	-----MEIRCTEEGAGPGIFRMELGDQOSISQSQ			
gi 14770563	MSLMDDQPPMEAOYAEEGPGPGIFRAEPGDQOHPIISOAV			
gi 12248777	-----			
	50	60	70	80
NOV10a
NOV10b	CWRSMRGCAVLGALGLLAGAGVGSWLLVLYLCPAASQPI			
gi 13540535	CWRSMRGCAVLGALGLLAGAGVGSWLLVLYLCPAASQPI			
gi 13878822	RWCCLRGCVILGVLLGLLAGAGIASWLLVLYLWPAASPSI			
gi 13507652	RWCCLRGCVILGVLLGLLAGAGIASWLLVLYLWPAASPSI			
gi 14770563	CWRSMRGCAVLGALGLLAGAGVGSWLLVLYLCPAASQPI			
gi 12248777	-----			

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```
          90      100      110      120
NOV10a    SGTLODEEETLSCSEASAEALLPALPKTVSFRINSEDFL
NOV10b    SGTLODEEETLSCSEASAEALLPALPKTVSFRINSEDFL
gi 13540535 SGTLODEEETLSCSEASAEALLPALPKTVSFRINSEDFL
gi 13878822 SGTLODEEETLSCSEASAEALLPALPKTVSFRINSEDFL
gi 13507652 SGTLODEEETLSCSEASAEALLPALPKTVSFRINSEDFL
gi 14770563 SGTLODEEETLSCSEASAEALLPALPKTVSFRINSEDFL
gi 12248777 SGTLODEEETLSCSEASAEALLPALPKTVSFRINSEDFL
```

```
          130      140      150      160
NOV10a    LEAQVRDQPRWLLVCHEGWSPALGTOICWSLGHTRLTTHK
NOV10b    LEAQVRDQPRWLLVCHEGWSPALGTOICWSLGHTRLTTHK
gi 13540535 LEAQVRDQPRWLLVCHEGWSPALGTOICWSLGHTRLTTHK
gi 13878822 LOVQVRAPDWLLVCHEGWSPALGTHICKSLGHTRLTTHK
gi 13507652 LOVQVRAPDWLLVCHEGWSPALGTHICKSLGHTRLTTHK
gi 14770563 LEAQVRDQPRWLLVCHEGWSPALGTOICWSLGHTRLTTHK
gi 12248777 LEAQVRDQPRWLLVCHEGWSPALGTHICKSLGHTRLTTHK
```

```
          170      180      190      200
NOV10a    GVNLDIKLNSQOFAQLSPRLGGFEEAWQPSRTTEAVR
NOV10b    GVNLDIKLNSQOFAQLSPRLGGFEEAWQPSRTTEAVR
gi 13540535 GVNLDIKLNSQOFAQLSPRLGGFEEAWQPSRTTEAVR
gi 13878822 AVNLSDIKLNSQOFAQLSARPGGLVEEAWQPSRTTEAVR
gi 13507652 AVNLSDIKLNSQOFAQLSARPGGLVEEAWQPSRTTEAVR
gi 14770563 GVNLDIKLNSQOFAQLSPRLGGFEEAWQPSRTTEAVR
gi 12248777 AVNLSDIKLNSQOFAQLSARPGGLVEEAWQPSRTTEAVR
```

```
          210      220      230      240
NOV10a    NNCTSGGVVSLRCSECGARPLASRIVGGQSVAPGRWPWOA
NOV10b    NNCTSGGVVSLRCSECGARPLASRIVGGQSVAPGRWPWOA
gi 13540535 NNCTSGGVVSLRCSECGARPLASRIVGGQSVAPGRWPWOA
gi 13878822 ANCPSGRIVSLRCSECGARPLASRIVGGQSVAPGRWPWOA
gi 13507652 ANCPSGRIVSLRCSECGARPLASRIVGGQSVAPGRWPWOA
gi 14770563 NNCTSGGVVSLRCSECGARPLASRIVGGQSVAPGRWPWOA
gi 12248777 ANCPSGRIVSLRCSECGARPLASRIVGGQSVAPGRWPWOA
```

```
          250      260      270      280
NOV10a    SVALGRHTCGGSVLAPRWVVTAAHCMISFRLARLSSWRV
NOV10b    SVALGRHTCGGSVLAPRWVVTAAHCMISFRLARLSSWRV
gi 13540535 SVALGRHTCGGSVLAPRWVVTAAHCMISFRLARLSSWRV
gi 13878822 SVMLGSRHTCGASVLAPRWVVTAAHCMISFRLARLSSWRV
gi 13507652 SVMLGSRHTCGASVLAPRWVVTAAHCMISFRLARLSSWRV
gi 14770563 SVALGRHTCGGSVLAPRWVVTAAHCMISFRLARLSSWRV
gi 12248777 SVMLGSRHTCGASVLAPRWVVTAAHCMISFRLARLSSWRV
```

```
          290      300      310      320
NOV10a    HAGLVSHSAVRPHOGATVERIIPHPLYSAQNHDYDVALLR
NOV10b    HAGLVSHSAVRPHOGATVERIIPHPLYSAQNHDYDVALLR
gi 13540535 HAGLVSHSAVRPHOGATVERIIPHPLYSAQNHDYDVALLR
gi 13878822 HAGLVSHSAVRPHOGATVERIIPHPLYSAQNHDYDVALLR
gi 13507652 HAGLVSHSAVRPHOGATVERIIPHPLYSAQNHDYDVALLR
gi 14770563 HAGLVSHSAVRPHOGATVERIIPHPLYSAQNHDYDVALLR
gi 12248777 HAGLVSHSAVRPHOGATVERIIPHPLYSAQNHDYDVALLR
```

```
          330      340      350      360
NOV10a    LQTAENFSDTVGAVCLPAKEQEFPKGSECVWSGWGHTHPS
```

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NOV10b      LQTALNFSDTVGA VCLPAKEQHFPPKGSRCWVSGWGHTDPS
gi | 13540535 | LQTALNFSDTVGA VCLPAKEQHFPPKGSRCWVSGWGHTDPS
gi | 13878822 | LRTPI NFSDTVDA VCLPAKEQHFPPWGSRCWVSGWGHTDPS
gi | 13507652 | LRTPI NFSDTVGA VCLPAKEQHFPPWGSRCWVSGWGHTDPS
gi | 14770563 | LQTALNFSDTVGA VCLPAKEQHFPPKGSRCWVSGWGHTDPS
gi | 12248777 | LRTPI NFSDTVDA VCLPAKEQHFPPWGSRCWVSGWGHTDPS

```

```

          370      380      390      400
.....|.....|.....|.....|.....|.....|
NOV10a      HTYSSDMLQDTMVPLLS TQLCNSSCVYSGALT PPRMLCAGY
NOV10b      HTYSSDMLQDTMVPLLS TQLCNSSCVYSGALT PPRMLCAGY
gi | 13540535 | HTYSSDMLQDTMVPLLS TQLCNSSCVYSGALT PPRMLCAGY
gi | 13878822 | HTYSSDMLQDTMVPLLS TQLCNSSCVYSGALT PPRMLCAGY
gi | 13507652 | HTYSSDMLQDTMVPLLS TQLCNSSCVYSGALT PPRMLCAGY
gi | 14770563 | H-----S-----LQLG Y
gi | 12248777 | HTYSSDMLQDTMVPLLS TQLCNSSCVYSGALT PPRMLCAGY

```

```

          410      420      430      440
.....|.....|.....|.....|.....|.....|
NOV10a      LDGRADACQGD SGGPLVCPD GDTWRLVG VSWGRGCAEPN
NOV10b      LDGRADACQGD SGGPLVCPD GDTWRLVG VSWGRGCAEPN
gi | 13540535 | LDGRADACQGD SGGPLVCPD GDTWRLVG VSWGRGCAEPN
gi | 13878822 | LDGRADACQGD SGGPLVCPD GDTWRLVG VSWGRGCAEPN
gi | 13507652 | LDGRADACQGD SGGPLVCPD GDTWRLVG VSWGRGCAEPN
gi | 14770563 | APG-----HCGALVQHS---ALQQLRVOR---SPH
gi | 12248777 | LDGRADACQGD SGGPLVCPD GDTWRLVG VSWGRGCAEPN

```

```

          450      460      470
.....|.....|.....|.....|.....|.....|
NOV10a      HPGVYAKVAEFLDWIHD TACVSVGAGVQGDF (SEQ ID NO:27)
NOV10b      HPGVYAKVAEFLDWIHD TACDSLL----- (SEQ ID NO:29)
gi | 13540535 | HPGVYAKVAEFLDWIHD TACDSLL----- (SEQ ID NO:71)
gi | 13878822 | RPGVYAKVAEFLDWIHD TVQVR----- (SEQ ID NO:72)
gi | 13507652 | RPGVYAKVAEFLDWIHD TVQVR----- (SEQ ID NO:73)
gi | 14770563 | PP-----HALRWLPGRKG----- (SEQ ID NO:74)
gi | 12248777 | RPGVYAKVAEFLDWIHD TVQVR----- (SEQ ID NO:75)

```

At page 116, please replace Table 10H with the following:

Table 10H Domain Analysis of NOV10

gnl|Smart|smart00020, Tryp_SpC, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues. (SEQ ID NO:96)
CD-Length = 230 residues, 100.0% aligned
Score = 266 bits (681), Expect = 2e-72

```

Query:  224  RIVGGQSVAPGRWPQASVAL-GFRHTCGGSVLAPRWVVTAAHCMHSFRLARLSSWRVHA  282
          |||||  | +|||  +  | || |||+++|||+|||++  || ||
Sbjct:   1    RIVGGSEANIGSFPPQVSLQYRGGRHFCGGSLLSPRWVLTAAHCVYGSAP---SSIRVRL  57

Query:  283  GLVSHSAVRPHQALVERIIPHPLYSAQNHDYDVALLRLQTALNFSDTVGA VCLPAKEQH  342
          |  +  |  ++|  ||  +  +|  +|||+|  +  ||||  +|||+  +
Sbjct:  58    GSHDLSSGEETQTVKVKVIVHPNYPSTYDNDIALKLSEPVTLSDTVVRPICLPSSGYN  117

Query:  343  FPKGSRCWVSGWGHTHPSHTYSSDMLQDTMVPLLS TQLCNSSCVYSGALT PPRMLCAGYLD  402

```


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```

      | |+ | |||| | | | ||+ ||++| | + |+ | |||| |+
Sbjct: 118 VPAGTTCTVSGWGRTSESSGSLPDTLQEVNVPVIVSNATCRRAYSGGPAITDNMLCAGGLE 177

Query: 403 GRADACQGDSSGGPLVCPDGDWTWRLVGVVSWGR-GCAEPNHGPGVYAKVAEFLDWI 455
      | ||||| ||||| + | |||+||| ||| || ||||| ++ +|||
Sbjct: 178 GGDACQGDSSGGPLVC-NDPRWVLVGIVSWGSGYGCARPKNKPGVYTRVSSYLDWI 230
```

Query: (of SEQ ID NO:27)

Sbjct: (SEQ ID NO:96)

At page 116, please replace Table 10I with the following:

Table 10I. Domain Analysis of NOV10

gnl|Pfam|pfam00089, trypsin, Trypsin. Proteins recognized include all proteins in families S1, S2A, S2B, S2C, and S5 in the classification of peptidases. Also included are proteins that are clearly members, but that lack peptidase activity, such as haptoglobin and protein Z (PRTZ*). (SEQ ID NO:97)
CD-Length = 217 residues, 100.0% aligned
core = 211 bits (538), Expect = 6e-56

```

Query: 225 IVGGQSVAPGRWPWQASVALGFRHTCGGSVLAPRWVVTAAHCMHSFRLARLSSWRVHAGL 284
      |||+ | +||| |+ + | |||+++ ||+|||+ | | |
Sbjct: 1 IVGGREAQAGSFPPWQVSLQVSSGHFCGGS LI SENWVLTAAHCVSG-----ASSVRVVLGE 55

Query: 285 VSHSAVRPH-QGALVERIIPHPLYSAQNHDYDVALLRQLTALNFSDTVGA VCLPAKEQHF 343
      + | ++|| || |+ | +|||+|++ + ||| +|||+
Sbjct: 56 HNLGTTEGTEQKFDVKKIIVHPNYPNDT--NDIALLLKLSPVTLGDTV RPICLP SASSDL 113

Query: 344 PKGSR CWVSGWGHTHPSHTYSSDMLQDTVVP LLSTQLCNSSCVYSGALTPRMLCAGYLDG 403
      | |+ | |||| | + +|| ||+ |||++| + | |+ | | +| +||| |
Sbjct: 114 PVGTTCSVSGWGRTK--NLGTSDTLQEVVVPVIVSRETCSR A--YGGTVTDTMICAGALGG 169

Query: 404 RADACQGDSSGGPLVCPDGDWTWRLVGVVSWGRGCAEPNHGPGVYAKVAEFLDWI 455
      + ||||| ||||| || |||+||| ||| |+||| ++ +|||
Sbjct: 170 K-DACQGDSSGGPLVCSDG---ELVGIVSWG YGCAVGNYPGVYTRVSR YLDWI 217
```

Query: (of SEQ ID NO:27)

Sbjct: (SEQ ID NO:97)